



# **STIC Search Report**

## **Biotech-Chem Library**

STIC Database Tracking Number: 182281

TO: **Phuong Bui**  
Location: **REM/2A15/2C18**  
Art Unit: **1638**  
Friday, March 17, 2006  
Case Serial Number: **09/938294**

From: **Barb O'Bryen**  
Location: **Biotech-Chem Library**  
Remsen 1a69  
Phone: **571-272-2518**

*BOB*  
**barbara.obryen@uspto.gov**

### Search Notes

# RUSH

**This Page Blank (uspto)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 23:57:28 ; Search time 8728 Seconds  
(without alignments)  
11084.734 Million cell updates/sec

Title: US-09-938-294-2  
Perfect score: 1702  
Sequence: 1 attcgctcgagtttgatcc.....gaggagatttcaatcttagt 1702

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :		GenEmbl:*	
		1: gb_ba.*	
		2: gb_in.*	
		3: gb_env.*	
		4: gb_om.*	
		5: gb_ov.*	
		6: gb_pat.*	
		7: gb_ph.*	
		8: gb_pr.*	
		9: gb_ro.*	
		10: gb_sts.*	
		11: gb_sy.*	
		12: gb_un.*	
		13: gb_vi.*	
		14: gb_htg.*	
		15: gb_pl.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		SUMMARIES	
No.	Score	Match	Length DB ID	Description	
1	1019.4	59.9	1120 15	BT017155 Zea mays	
2	664	39.0	2069 15	BT013466 Lycopersi	
3	602.4	35.4	1695 15	AK176263 Arabidops	
4	602.4	35.4	1709 15	AK176210 Arabidops	
5	590.8	34.7	1765 15	BT008621 Arabidops	
6	282.6	16.6	90341 15	AC024609 Arabidops	
7	282.6	16.6	119942 15	AC007797 Arabidops	
8	253.4	14.9	100685 15	AC023754 Arabidops	
9	224.8	13.2	110000 15	Continuation (89 o	
10	224.8	13.2	146081 15	AP001366 Oryza sat	
11	158.6	9.3	92376 14	AP008071 Lotus cor	
12	115.2	6.8	92376 14	AP008071 Lotus cor	
13	93	5.5	2013 15	BT008418 Arabidops	
14	93	5.5	2603 15	BT002514 Arabidops	
15	90.2	5.3	1172 15	AK221889 Arabidops	
16	89.4	5.3	2124 15	ATH507211 Arabidops	
17	89.4	5.3	2557 15	AY091763 Arabidops	
18	87.8	5.2	75948 15	AC037424 Arabidops	

C 19	87.8	5.2	117737	15	F6D8	AC008016 Arabidops
C 20	65.8	3.9	147292	14	AC023010	AC023010 Homo sapi
21	60	3.5	5445	15	AK121451	AK121451 Oryza sat
22	60	3.5	110000	15	AP008209_023	Continuation (24 o
23	60	3.5	150503	15	AC122149_	AC122149 Oryza sat
24	58.2	3.4	42273	15	NCB12N19	AL669987 Neurospor
25	58.2	3.4	122151	15	NCB23H20	AL669988 Neurospor
C 26	56.4	3.3	35762	15	AB026653	AB026653 Arabidops
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28	56	3.3	70311	15	AF128457	AF128457 Oryza sat
29	56	3.3	77605	15	AF119222	AF119222 Oryza sat
C 30	56	3.3	110000	15	AP008217_233	Continuation (234
31	56	3.3	142852	15	AF161269	AF161269 Oryza sat
C 32	55.6	3.3	48144	14	AC069166	AC069166 Homo sapi
33	54.4	3.2	1555	15	AK106377	AK106377 Oryza sat
C 34	54	3.2	85813	15	AP006644	AP006644 Lotus cor
C 35	53.6	3.1	129986	14	AC148571	AC148571 Taeniopvg
36	53.2	3.1	110000	15	AE017348_09	Continuation (10 o
37	53.2	3.1	110000	15	AE017348_10	Continuation (11 o
38	53.2	3.1	148061	14	CR848712	CR848712 Danio rer
C 39	53	3.1	110000	15	AP008217_017	Continuation (18 o
C 40	53	3.1	149493	15	AC123528	AC123528 Oryza sat
C 41	53	3.1	305296	14	AC152796	AC152796 Bos tauru
42	53	3.1	321250	1	SC0939111	AL939111 Streptomy
C 43	53	3.1	345865	14	AC152789	AC152789 Bos tauru
C 44	52	3.1	956	10	PM2D12B	AL684743 Penicilli
45	52	3.1	2037	15	AK120574	AK120574 Oryza sat

ALIGNMENTS

RESULT 1	BT017155	1120 bp	mRNA	linear	PLN 27-OCT-2004
LOCUS	Zea mays clone EL01N0367F09.c	mRNA sequence.			
DEFINITION	BT017155				
ACCESSION	BT017155				
VERSION	BT017155.1	GI:54651936			
KEYWORDS	FLI_CDNA.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X., Larkins, B., Becraft, P. and Messing, J.				
TITLE	Characterization of the maize endosperm transcriptome and its comparison to the rice genome				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1120)				
AUTHORS	Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X., Larkins, B., Becraft, P. and Messing, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190 Frelinghuysen Rd, Piscataway, NJ 08854, USA				
FEATURES	Location/Qualifiers				
Source	1..1120				
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	/clone="EL01N0367F09.c"				
ORIGIN					
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Best Local Similarity	97.7%;	Pred. No.	2.1e-194;		
Matches	1058;	Conservative	0;	Mismatches	16; Indels 9; Gaps 2;
QY	575	GAAGATCATGTTCTTAAAGTCCTTCGAGAGATTTTGTGGTCCATGAAATGCGTGG	634		
Db	9	GATAGATCATGTTCTTAAAGTCCTTCGAGAGATTTTGTGGTCCATGAAATGCGTGG	68		
QY	635	GCATTACTTTAAGGTTGAATATGTCAACATCTTCCCTTTGTGCTGGAGCCATGATTGA	694		

||||| 69 GCATTACTTTAAGGTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGA 128

QY 695 TTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCCTGAAATACAGAT 754

Db 129 TTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCCTGAAATACAGAT 188

QY 755 GCCACAAACTTATGTTGTTACCTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGA 814

Db 189 GCCACAAACTTATGTTGTTACCTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGA 248

QY 815 CAATGTCGAAGAGAGTCTTACGGGAACATATTCGTGAATCCCTTGGAGTACGGAGTGA 874

Db 249 CAATGTCGAAGAGAGTCTTACGGGAACATATTCGTGAATCCCTTGGAGTACGGAGTGA 308

QY 875 GGATCTCCTGTTTGCAATAATAAACAGTGTATCACGAGGAAGGGACAAAGACTTATTCT 934

Db 309 GGATCTCCTGTTTGCAATAATAAACAGTGTATCACGAGGAAGGGACAAAGACTTATTCT 368

QY 935 TCAAGCATTTTATCAGGCTTTGACGCTCATCAACACGAGAAACTTAAAGTGCCTAGAAAT 994

Db 369 TCAAGCATTTTATCAGGCTTTGACGCTCATCAACACGAGAAACTTAAAGTGCCTAGAAAT 428

QY 995 ACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAATTTGAGACTCAGTTACG 1054

Db 429 ACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAATTTGAGACTCAGTTACG 488

QY 1055 TGACTTTGTGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGC 1114

Db 489 TGACTTTGTGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGC 548

QY 1115 AGTGGCCCTTACTTTGGCAGCAATTGATGTGTTTGTTCAGAAATTCACGGCCGTGGAGA 1174

Db 549 AGTGGCCCTTACTTTGGCAGCAATTGATGTGTTTGTTCATAAATTCACGGCCGTGGAGA 608

QY 1175 ATGCTTTGGAAGGATAACAATTGAAGCAA-TGGCATTCAGTTGCCAGTATTGGGCACGG 1233

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QY 1234 CTGCTGGAGGGACACGGAGATCGTCTGGACGGCTCGACTGGCCCTTCGCACTCCTGCTG 1293

Db 669 CTGCTGGAGGGACACGGAGATCGTCTGGACGGCTCGACTGGCCCTTCGCACTCCTGCTG 728

QY 1294 GGAAGGAGGGCGTGGCGCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGC 1353

Db 729 GGAAGGAGGGCGTGGCGCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGC 788

QY 1354 AGAGGGTCTCCATGGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGTTTCATGGAGCAC 1413

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QY 1414 ACATGGCTGAGAGGATCGCGCGGTGTTGAAGGATGTCCTGAGGAAATCACAGGAGCACT 1473

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QY 1474 CCAGGTCTTGAGCTTTGCCGTGCCCATCAGCTTGGCGCTAACATGTTGAACTAGATTTTAC 1533

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QY 1534 GGGCTACGCCTACGTGTTGAGGCTGTAAACTGTAGATTGCACCTCTGTGTTGCTACTTTT 1593

Db 969 GAGCTACGCCTACGTGTTGAGGCTGTAAACTGTAGATTGCACCTCTCTGTTGCTACTCCTT 1028

QY 1594 TCACATTCA-----TGTTTACCTATTAGGCGATGTCCGATTCTATTCCAATTTCATA 1645

Db 1029 TCACATTCAATTGCTCTGTTGTTTACCTATTAGGCTTTGTCTGGTTCTACGGCAATTTCATA 1088

QY 1646 TAG 1648

Db 1089 TAG 1091

BT013466 2069 bp mRNA linear PLN 11-MAY-2004

LOCUS Lycopersicon esculentum clone 132125F, mRNA sequence.

DEFINITION

BT013466

BT013466

BT013466.1 GI:47104881

FLI\_CDNA.

KEYWORDS

SOURCE Lycopersicon esculentum (Solanum lycopersicum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE

1 (bases 1 to 2069)

Kirkness,B.F., Wang,W. and Vazeille,A.

AUTHORS Direct Submission

TITLE Submitted (11-MAY-2004) The Institute for Genomic Research, 9712

JOURNAL Medical Center Drive, Rockville, MD 20850, USA

FEATURES

Location/Qualifiers

1..2069

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/db\_xref="taxon:4081"

/clone="132125F"

/tissue type="fruit"

/note="TZXBC20"

ORIGIN

Query Match 39.0%; Score 664; DB 15; Length 2069;

Best Local Similarity 71.4%; Pred. No. 6.1e-123;

Matches 874; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

QY 266 GAGTCCCTCGGGTTCATGAGGTCGAAGTCGTGCTCCTCGTCTCCCATGAGCTCTCCCT 325

Db 622 GAGCCCACTCAGTTTCATGAAGCTAGGCTTGTGCTTCTTGCTCCCATGAGCTTTCCCT 681

QY 326 CTCTGTTGCTCCACTTTTACTGATGGAATTAGCATTTCTCTGAGGCATGTTGGCTCGCA 385

Db 682 TTCTGTTGGACCTCTGTTGTTGATGGAGCTGGCATTTTGTGAGAGGTGTTGGTCTGA 741

QY 386 AGTGGTGTGGATAACAACCAGAGATCACAAAGAAACAAATGATGTCACATATAGCTTGA 445

Db 742 AGTCTGTTGGATCACAAATCAAAGGCCATCTGAAACAAATAACATGTATACAGTTTGA 801

QY 446 GCATAGGATGTTGAACCATGGAGTGCAGGTTTACCAGCTAGAGGACAGGAGGCAGTTGA 505

Db 802 GCACAAATGTTACACCGAGGAGTTCAGGTTGTTCTCTCGAAGGCCAGGAGGCAATGA 861

QY 506 TATTGCTCTAAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGCGCAAGTGGCTTGA 565

Db 862 TACTGCTTTGAAAGCTGACTTGGTTGTTTAAACACTGCCGTTGCTGGGAAATGTTTGA 921

QY 566 CCTGTTCTGAAAGATCATGTTCTTAAAGTCCCTCCGAAGATTTGTGGTGGATCCATGA 625

Db 922 TGCTGTTCTTAAGGAACACGTTTCTGAAGTCCCTCCCAAAGTTTGTGGTGGATCCATGA 981

QY 626 AATGCGTGGGCATTACTTTAAGGTTGAATATGTCAAAACATCTTCCCTTTGTTGCTGGAGC 685

Db 982 AATGCGCGTCACTTACTTCAGTCTAGATTATGTGAAACACCTTCCCATATGTTGCTGTGC 1041

QY 686 CATGATTGATTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCCTGAA 745

Db 1042 AATGATTGATTACATGTAAACAGCTGAATACTGGAAGAAATAGGACACAGGAACGGCTAAG 1101

QY 746 AATACAGATGCCACAAACTTATGTTGTTTACCTGGGGAATAGTAAAGAACTAATGGAAGT 805

Db 1102 GATCAAAATGCCAAACCCCATGTCGTTTCATCTTGGCAACAGCAATGAGCTAATGGAAAT 1161

QY 806 TGCTGAAGCAATGTGCAAGAAGAGTCTTACGGGAACATATTCGTGAATCCCTTTGGAGT 865

Db 1162 TGCTGAAGATAGTGTGGCAAAAGGATTTTGAGGGAGCATGTTCTGTAATCTCTTTGGAGT 1221

QY 866 ACGGAGTGAGGATCTCTGTTTGGCAATAATAAACAGTGTATCACGAGGAAAGGACAAGA 925

Db 1222 TCGAAACGAAGATATACTGTTTCTCCCTCATAAATAGTGTACTCTGTTGGGAGGGTCAAGA 1281



QY 926 CTTATTCTTCAAGCATTTTATCAGGCTTTGTCAGCTCATCCACACGAGAACTTAAAGT 985  
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Db 1282 CTTATTCTTACGGTCGTTTATGAGAGCTTGCAGATTATTCAAGAACGGAAGTTACAATT 1341  
986 GCCTAGATACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAAATTTGAGAC 1045  
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Db 1342 ACCATCAATTCAATGCTGTTGTTGTAGGAGTGACATGACTAGTATAGTAAATTTGAGAC 1401  
1046 TCAGTTACGTGACTTTTGTGGTGAAGAACACGATTTCATGACCGTGTCCTATTTTGTGAACAA 1105  
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Db 1402 AGAGCTTAGGAACCTTTGTCATATCAAGAAGATCCAGAATTATGTTTCATTTTGTAAATAA 1461  
1106 GACATTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAAATTCACAGG 1165  
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Db 1462 GACACTGACGGTAGCCCCCATATCTTGTGCAGTTGATGTTCTTGTTCAGAAATTCACAGG 1521  
1166 CCGTGGAGATGCTTTGGAAGGATAACAATGAAGCAATGGCAATGCCAGTTGCCAGTATT 1225  
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Db 1522 ACGAGGTGAATGCTTTGGTAGGATTACTATTGAGGCGATGGCGTTTCAGCTGCCTGTGTT 1581  
1226 GGGCACGGCTGCTGGAGGGACCCAGGAGATCGTCTGACGGCTCGACTGGCCTTCTGCA 1285  
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Db 1582 GGGAACTGCTGCTGGTGGCACCCCAAGAAATGTAACAAATGGACAACTGGTCTTCTYACA 1641  
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1346 CGCCGAGCAGAGGGTCTCCATNGGGGAAAGGGCTATGGCAGGTTGAAGGAAATGTTTCAT 1405  
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Db 1702 CGTTGAGAGAGGCTTACAAATGGGTAAAGGATGATGAGAGGTTAAAGAGACTTTTCT 1761  
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Db 1762 GGAGCATCATGGAAGAAAGAAATTGCAGGAGTTCTAAAGGACGTGTTGCAAAAAGCAAT 1821  
1466 GGAGCACTCCAGGTCTTGAGCTTT 1489  
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Db 1822 GGAACATCAAGGACATGATAATT 1845

RESULT 3  
AK176263  
LOCUS Arabidopsis thaliana mRNA for hypothetical protein, complete cds, 1695 bp mRNA linear PLN 09-SEP-2004  
DEFINITION clone: RAFL23-16-P14.  
ACCESSION AK176263  
VERSION AK176263.1 GI:51970667  
KEYWORDS FLI CDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1  
Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A.,  
Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K.,  
Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K.,  
Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P.,  
Kawai,J., Hayashizaki,Y. and Shinozaki,K.  
Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs  
Unpublished  
2 (bases 1 to 1695)  
Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A.,  
Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K.,  
Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K.,  
Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P.,  
Kawai,J., Hayashizaki,Y. and Shinozaki,K.  
Direct Submission  
Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences  
Center, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa  
230-0045, Japan (E-mail:mseki@gsc.riken.jp,

URL:http://range.gsc.riken.jp/, Tel:81-45-503-9625,  
Fax:81-45-503-9586)  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al. (1998) Plant J. 15:707-720;  
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI  
and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et  
al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This  
clone is in a modified pBluescript vector.  
Please visit our web site (http://range.gsc.riken.jp/) for further  
details.

FEATURES  
source  
Location/Qualifiers  
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WKNRTHDLRGIKMPKTYVVLHNSKELMEVADSPAKNVLREQVRESLGVNEDILFG  
IINSVSRGKGQDLFLRAFPHESLKVIVETKLEVTMHAVVVGSMDMSAQTKEFETELNPF  
VQEMKLOKIVHFVNKTMKVAPYLAADVLVONSQARCECFGRITIEAMAFKLPVLGTA  
AGGTMEIVVNRITGLLHNTGKDGVLPLAKNIVKLATNVKWRNTMGKKGYERVKEMFELE  
HMSHRIASVLRVLQHAKIHSRTTNSDH"

ORIGIN

Query Match 35.4%; Score 602.4; DB 15; Length 1695;  
Best Local Similarity 69.1%; Pred. No. 1.5e-110;  
Matches 838; Conservative 0; Mismatches 371; Indels 3; Gaps 1;  
QY 266 GAGTCCCTCGGGTTCATGAGTCCAAAGCTCGTGCTCCTCGTCTCCCATGAGCTCTCCCT 325  
Db 289 GAATCCTCTCGAGTTCATGAATCAAAGCTCGTTTACTTGTCTCATGAACCTCTCGCT 348  
QY 326 CTCTGCTGCTCCACTTTTACTGATGAATTAGCATTTCTCTGAGGCATGTTGGCTCGCA 385  
Db 349 CTCAGGTGGACCTTTATTGTTAATGGAATTGGCGTTTGTCTTAGAGGAGTTGAATCTGA 408  
QY 386 AGTGGTGTGGATAACAACACAGAGATCACAAGAAACAATGATGTACATATAGCTTGA 445  
Db 409 AGTTGTTGGATCAGGAATCAGAAACACAGTTGAAGAGATGAAGTATCAAGTTCTAGA 468  
QY 446 GCATAGGATGTTGAACCATGAGTGCAGGTTTTTACCAGCTAGAGGACAGGAGGAGTTGA 505  
Db 469 ACACAAGATGTTGGATCGAGGAGTCCAGGTGATATCAGCAAAAGATCAGAAAGCTATAGA 528  
QY 506 TATTGCTCTAAAAGCTGATCTGTTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGA 565  
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QY 566 CCCTGTTCTGAAAGATCATGTTCTTAAAGTCCCTCCGAAGATTTTGTGGTGGATCCATGA 625  
Db 589 TGCAGTTCTCAAGGACAAATGTTCTTAAAGTCTTCTTAAAGTACTCTGGTGGATTCATGA 648  
QY 626 AATGCTGGGCATTACTTTAAGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGC 685  
Db 649 GATGAGAGGTCACTATTTCAAACCCGGATTTAGTCAAGCACCTTCCGTTTGTTCAGGTGC 708  
QY 686 CATGATTGATTCTCATACACGGCTGAGTATTGGAATAGAGGACTAGCGATCGCCTGAA 745  
Db 709 TATGATTGATTCCGACCGCAACAGCTGAATACTGGAAGAACAGAACTCATGATCGCTTAGG 768









Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.

Direct Submission

Submitted (11-AUG-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE

AUTHORS

5 (bases 1 to 90341)  
Fegerspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.

Direct Submission

Submitted (12-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT

On Mar 9, 2000 this sequence version replaced gi:7121532.  
Bases 1-59,676 of IGF clone F14P1 overlap with IGF clone F6F9, gb|AC007797.

e-mail for correspondence: arab@sequence.stanford.edu  
Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).  
Location/Qualifiers

FEATURES

source

1. 90341  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/chromosome="1"  
/clone="F14P1"  
1. 59676  
/note="overlap with IGF clone F6F9, gb|AC007797, see GenBank record for BAC clone F6F9 for annotation in this region."

misc\_feature

gene

join(60210..60507,60608..60778,60878..60927,61025..61081,61184..61249,61387..61461,61599..61717,61807..61960)  
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PKTVSKIHLGNKYQNKLLIEMIDASQLPDFGGTCTCADGGCMRSKDGKWKDSEILK  
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KIGSVRHIWSWLTAFPISTFTLLASLALPQTKEKSLQSHSSVRAELCDERIAESRPP  
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80606..80776

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Db	46971	TTCAGGTGATATCAGCAAGAGTCAAGAAAGCTATAGATACAGCTCTCAAGTCTGATCTGG 46912
QY	529	TTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTGAAAGATCATGTTT 588
Db	46911	TTGTTTTAAACACTGCTGTTGCTGGGAAATGGCTTGATGTCAGTTTCTCAAGGACAAATGTT 46852
QY	589	CTAAAGTCTTCCGAAGATTTTGTGTGGATCCATGAAATGCGTGGGCATTACTTTAAGG 648
Db	46851	CTAAAGTCTTCTCTAAAGTACTCTGTGGATTCATGAGATGAGAGTCACTATTTCAAAC 46792
QY	649	TTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGAATCTCATACAACGG 708
Db	46791	CGGATTTAGTCAAGCACCTTCGGTTTGTGTCAGGTGCTATGATTGATTCGCACGCAACAG 46732
QY	709	CTGAGTATTGGAATAGCAGGACTAGCGATCGC----- 740
Db	46731	CTGAATACTGGAAGAACAGAACTCATGATCGCTTAGGGTCTGTTTCCTCTCTGTAGAGTC 46672
QY	741	----- 740
Db	46671	TTGCGATATATTAGTTTACGTTATTGTTCATAAGCTTAACAGTGTTTATTCTTTATTGTT 46612
QY	741	----CTGAAATACAGATGCCACAACTTATGTTTGTTCACCTGGGGAATAGTAAAGAACT 796
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QY	797	AATGGAAGTTGCTGAAGACAATGTCGCAAGAGAGTCTACGGGAACATATTTCGTGAATC 856
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QY	901	----- 900
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QY	901	-----GTGTATCACGAGGAAGGGACAAG 924
Db	46371	TTAATTTGCTTTCTGACTGGTGCTTCTCTTATGTCAGGTGTATCTCGAGGAAGGGCCAAG 46312
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QY	1042	AGACTCAGTTACGTGACTTTTGTGGTGAAGAACACGATTCATGACCGGTGCTCCATTTTGTA 1101
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QY	1102	ACAAGACATTGGCAGTGGCCCTTACTTTGGCAGCAATTGATGTGCTTGTTCAGAAATCTC 1161
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QY	1162	AGGCGCGTGGAGAAATGCTTTTGAAGGATAACAATTGAAGCAATGGCATTTCAAGTTGCCAG 1221
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QY	1222	TATTGGGCACGGCTGCTGGAGGACCACGGAGATCGTCTCGACGGCTCGACTGGCCTTC 1281
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QY	1282	TGCATCCTGCTGGGAAGGAGGCGTGGCGCCTCTTTCACAAAGAACATCGTCAGACTCGCAA 1341
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QY	1342	GCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAAGGGCTATGCGCAGGGTGAAGGAAATGT 1401
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RESULT 7	AC007797	119942 bp	DNA	linear	PLN 12-SEP-2000
AC007797/c	Arabidopsis thaliana chromosome I BAC F6F9 genomic sequence,				
LOCUS	complete sequence.				
DEFINITION	AC007797				
ACCESSION	AC007797.7 GI:7839909				
VERSION	HTG.				
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis				
REFERENCE	1 (bases 1 to 119942)				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S., Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M., Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 119942)				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-JUN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA				
REFERENCE	3 (bases 1 to 119942)				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E., Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA				
REFERENCE	4 (bases 1 to 119942)				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.				



TITLE Direct Submission  
JOURNAL Submitted (12-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT On May 16, 2000 this sequence version replaced gi:7547094. Bases 60,267-119,942 of BAC clone F6F9 overlap with bases 1-59,676 of IGF clone F14P1, AC024609 and bases 1-3,490 of BAC clone F6F9 overlap with bases 89,221-92,710 of BAC clone T20H2, AC022472.

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Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.  
Direct Submission  
Submitted (13-SEP-2000) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

On Mar 9, 2000 this sequence version replaced gi:7143418.  
Bases 1-32,040 of IGF clone F1B16 overlap with bases 97,508-129,547 of IGF clone F10A5, gb|AC006434.

e-mail for correspondence: arab@sequence.stanford.edu  
Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev, http://genomic.sanger.ac.uk/gf/gf.shtml), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).

FEATURES

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complement(32986..33822)  
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CDS

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KPYLVGEVTWLEDRPSGENLDSLAEVEVLMKEVIRLSNRLNGKAEVQDLRRNQF  
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SSVSSNGSVLYCLEITKNYHSDSEIVDQVEIILMKLNFIPTSVFTTDLQYVDFDR  
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KNWDRSSAVTPDEEVFVLVALLRSALTGDEETQKLEYLKDQNRRILEFCEQAKINVQ  
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CDS

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CDS

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LQHAKARALR"

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CDS

59918..61713

/gene="F1B16.6"

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/note="Similar to homeodomain proteins"

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KQYKRCKNRVVDSYGESECEDFVFQKMGKREGKALKEASCSSKSSSKSFLKWHFAS  
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gene

complement(69063..69566)



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QY	1021	TTAATGCTCAGACCAAATTTGAGACTCAGTTACGTGACTTTGTGTGGAAGAACACGATTC 1080		AP008207_033	3300001	3410000
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QY	1081	ATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGCAATTG 1140		AP008207_035	3500001	3610000
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QY	1381	ATGGCAGGTTGAAGAAATGTTTCATGGAGCACCACATGGCTGAGAGGATCGCGCGGTGT 1440		AP008207_045	4500001	4610000
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Db 87824 GTTGCTGAAGATAATGTTGCAAGAAGAGTCCTACGGGAGCATATCCGTGAGTTCCTTGA 87765  
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Qy 901 ----- 900  
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Qy 901 -----GTGTATCAGGAGGAAGGACAAAGACTTATTCTTCAAGCATT 943  
Db 87644 TTGATGTTAAATACAGGTGTTTACGTGGAAGGCGGAGACTTATTCTTCAAGCGTT 87585  
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ORIGIN

Query Match 5.5%; Score 93; DB 15; Length 2603;  
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RESULT 15

AK221889  
LOCUS AK221889 1172 bp mRNA linear PLN 07-APR-2005  
DEFINITION Arabidopsis thaliana gene for hypothetical protein, partial cds,  
clone: RAFL22-26-A16.

ACCESSION

AK221889

VERSION

AK221889.1 GI:62321119

KEYWORDS

FLI CDNA.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A.,  
Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K.,  
Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K.,  
Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P.,  
Kawai,J., Hayashizaki,Y. and Shinozaki,K.  
Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs

TITLE

Unpublished

JOURNAL

2 (bases 1 to 1172)

REFERENCE

Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A.,  
Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K.,  
Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K.,  
Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P.,  
Kawai,J., Hayashizaki,Y. and Shinozaki,K.  
Direct Submission

TITLE

JOURNAL

Submitted (22-MAR-2005) Motoaki Seki, RIKEN Genomic Sciences  
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,  
230-0045, Japan (E-mail:mseki@gsc.riken.jp,  
URL:http://range.gsc.riken.jp/, Tel:81-45-503-9625,  
Fax:81-45-503-9586)

COMMENT

An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al. (1998) Plant J. 15:707-720;  
Seki et al. (2002) Science 296:141-145).

This clone is in a modified pBluescript vector.  
Please visit our web site (<http://range.gsc.riken.jp/>) for further  
details.

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match 5.3%; Score 90.2; DB 15; Length 1172;  
Best Local Similarity 53.6%; Pred. No. 1.3e-07;  
Matches 188; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

Qy	1116	GTGGCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAAATCTCAGGGCCGTGGAGAA	1175
Db	696	GTTGCCTCATTATACTCCGACGAGATGTCTACGTAACAAACTCCAGGGAGTTGGTGAA	755
Qy	1176	TGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCT	1235
Db	756	ACATTGGGAGAGTGACTATCGAAGCAATGGCTTATGGTCTTCCGGTCTTGGAACAGAT	815
Qy	1236	GCTGAGGGACACCGAGATCGTCTGGACGGCTCGACTGGCCTTCTGCATCCTGCTGGG	1295
Db	816	GCTGGAGGAACAAAGAGATAGTGGAGCAATGTTACAGGGCTACTTCTATCCTGTGGGG	875
Qy	1296	AAGGAGGCGTGGCGCCTCTTGCAAGAACAATCGTCAGACTCGCAAGCCACGCCGAGCAG	1355
Db	876	AGGCAGGTAACAAAGTTTGGCACAGAACTCTTTTGTCTTCTTAGAAACCCATCTACA	935
Qy	1356	AGGCTCTCCATGGGGGAAAGGGCTATGGCAGGTTGAAGGAATGTTTCATGGAGCACCAC	1415
Db	936	AGGCTACAACTAGGTAGCCAAGACGTGAAATCGTTGAGAAGATGTACATGAAGCAGCAC	995
Qy	1416	ATGCTGAGAGGATCGCGGCGGTGTTGAAGGATGTCCTGAGGAATCAGAG	1466
Db	996	ATGTACAAGAGATTGTGGATGTTCTAGTCAAATGTATGAGACACTAACTG	1046

Search completed: March 17, 2006, 02:40:37  
Job time : 8739 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 23:50:12 ; Search time 1063 Seconds  
(without alignments)  
10671.032 Million cell updates/sec

Title: US-09-938-294-2  
Perfect score: 1702  
Sequence: 1 attcggtcgagttgatcc.....gaggagatttcaatcttagt 1702

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues 9993994  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1647	96.8	1647	13	Adx09132 Plant ful
2	589.6	34.6	1715	3	Aac42068 Arabidops
3	426.2	25.0	1094	13	Adr65394 Cotton cd
4	262	15.4	276	7	Ads71019 Corn seed
5	257	15.1	257	7	Ads71062 Corn seed
6	244.8	14.4	948	13	Adr62845 Cotton cd
7	233	13.7	583	10	Abx56781 Arabidops
8	227	13.3	625	13	Adr62846 Cotton cd
9	227	13.3	625	13	Acn58791 Cotton gy
10	210	12.3	382	13	Adr65395 Cotton cd
11	158.6	9.3	514	13	Acn58833 Cotton gy
12	154.6	9.1	284	3	Aaa31140 Plant mic
13	74	4.3	1964	13	Adt18408 Plant cdn
14	67.4	4.0	254	9	Ada60128 Soybean s
15	67.4	4.0	254	12	Adq06025 Soybean t
16	52.4	3.1	2987	8	Abt17892 Aspergill
17	52.4	3.1	3495	8	Abt19706 Aspergill
18	50.4	3.0	90597	10	Adj72363 Streptomy
19	50.4	3.0	90600	6	Abq78872 S. roseos

C	20	50	2.9	6997	10	ADD29793	Add29793 Human tum
	21	49.8	2.9	912	3	AAZ93717	Aaz93717 HSV-1 V22
	22	49.2	2.9	1383	10	ADG33861	Adg33861 Actinomyc
	23	49	2.9	5877	6	ABS78681	Abs78681 Kitasatos
	24	49	2.9	5877	14	ABE12658	Aeb12658 Eneidiyne
	25	49	2.9	5877	14	AEC10251	Aec10251 Kitasatos
	26	48.6	2.9	872	13	ADx49110	Adx49110 Plant ful
	27	48.4	2.8	1076	2	AAZ30007	Aaz30007 Optimised
	28	48.4	2.8	1082	6	ABA92912	Aba92912 Organopho
	29	48.2	2.8	843	13	ADS15486	Ads15486 HSV-1 pol
	30	48.2	2.8	856	2	AAZ19784	Aaz19784 Herpes si
	31	48.2	2.8	856	2	AAZ07807	Aaz07807 HSV-1 teg
	32	48.2	2.8	900	3	AAA29395	Aaa29395 HSV-1 VP2
	33	48.2	2.8	903	6	ABV73163	Abv73163 Herpes si
	34	48.2	2.8	903	12	ADK68679	Adk68679 Epitope l
	35	48.2	2.8	903	12	ADQ10477	Adq10477 Herpes si
	36	48.2	2.8	903	13	ADS80957	Ads80957 Tumour as
	37	48.2	2.8	903	13	ADW76736	Adw76736 Human cyt
	38	48.2	2.8	906	13	ADS15488	Ads15488 HSV-1 pol
	39	48.2	2.8	912	2	AAx26227	Aax26227 HIV-1 VP2
	40	48.2	2.8	912	3	AAZ88468	Aaz88468 HSV-1 VP2
	41	48.2	2.8	912	4	AAF58996	Aaf58996 HSV-1 VP2
	42	48.2	2.8	912	6	ABA93386	Aba93386 HSV-1 VP2
	43	48.2	2.8	912	10	ADF70996	Adf70996 Phosphope
	44	48.2	2.8	912	12	ADM83002	Adm83002 Transcell
	45	48.2	2.8	950	2	AAV17085	Aav17085 Herpes si

ALIGNMENTS

RESULT 1

ADx09132

ID ADX09132 standard; cDNA; 1647 BP.

XX AC ADX09132;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polynucleotide seqid 3707.

XX KW plant protectant; plant growth regulant; gene therapy; plant;

XX KW recombinant DNA construct; physical array; plant breeding marker;

XX KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX KW extreme osmotic condition; pathogen tolerance; pest tolerance;

XX KW growth rate; cell cycle pathway; disease resistance;

XX KW galactomannan production; lignin production; plant growth regulator;

XX KW yield; plant growth; plant development; seed oil; protein yield;

XX KW protein content; gene; ss.

XX OS Unidentified.

XX PN US2004034888-A1.

XX PD 19-FEB-2004.

XX PF 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX PA (LIUJ/) LIU J.

XX PA (ZHOU/) ZHOU Y.

XX PA (KOVA/) KOVALIC D K.

XX PA (SCRE/) SCREEN S E.

XX PA (TABAY/) TABASKA J E.

XX PA (CAOY/) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX XX WPI; 2004-180133/17.

XX XX New recombinant DNA construct, useful for improving plant tolerance to

PT

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.

XX Claim 1; SEQ ID NO 3707; 15pp; English.

XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.

XX  
SQ Sequence 1647 BP; 400 A; 384 C; 440 G; 423 T; 0 U; 0 Other;

Query Match 96.8%; Score 1647; DB 13; Length 1647;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 ACCGGCGATGGCAAGACCCCGTCTCGCGGTGGCGGTCGCGGAGGCCCGGGCC 115  
DB 1 ACCGGCGATGGCAAGACCCCGTCTCGCGGTGGCGGTCGCGGAGGCCCGGGCC 60  
QY 116 GGTTCACAAACGGACCCAGCTCCTCCTCCTCGTGGCGCGTCCGAGCCTCCGCATC 175  
DB 61 GGTTCACAAACGGACCCAGCTCCTCCTCCTCGTGGCGCGTCCGAGCCTCCGCATC 120  
QY 176 CACAGCAGGGTTCCTCCTCGCGGTGCTCGAGACCCCTTGGAGCGCGTGGGACCC 235  
DB 121 CACAGCAGGGTTCCTCCTCGCGGTGCTCGAGACCCCTTGGAGCGCGTGGGACCC 180  
QY 236 CGCCGCCCTCAACACCGCGTCCGAGCGGAGTCCCTCGGGTTCATGAGTCCAAGCT 295  
DB 181 CGCCGCCCTCAACACCGCGTCCGAGCGGAGTCCCTCGGGTTCATGAGTCCAAGCT 240  
QY 296 CGTGCTCCTCGTCTCCCATGAGCTCCTCCTCCTCGTGGTCCACTTTACTGATGAATT 355  
DB 241 CGTGCTCCTCGTCTCCCATGAGCTCCTCCTCCTCGTGGTCCACTTTACTGATGAATT 300  
QY 356 AGCATTTCTCTGAGGCATGTTGGCTCGAAGTGGTGGATACAAACAGAGATCACA 415  
DB 301 AGCATTTCTCTGAGGCATGTTGGCTCGAAGTGGTGGATACAAACAGAGATCACA 360  
QY 416 AGAAACAAATGATGTACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGT 475  
DB 361 AGAAACAAATGATGTACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGT 420  
QY 476 TTTTACCAGCTAGAGGACAGGAGGCGAGTTCATATGCTCTAAAAGCTGATCTGTTATCTT 535  
DB 421 TTTTACCAGCTAGAGGACAGGAGGCGAGTTCATATGCTCTAAAAGCTGATCTGTTATCTT 480  
QY 536 AAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTGAAAGATCATGTTCCCTAAAGT 595  
DB 481 AAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTGAAAGATCATGTTCCCTAAAGT 540  
QY 596 CCTTCCGAAGATTTTGTGGTGGATCCATGAATCGTGGGCATTTCTTAAGTTGAATA 655  
DB 541 CCTTCCGAAGATTTTGTGGTGGATCCATGAATCGTGGGCATTTCTTAAGTTGAATA 600  
QY 656 TGTCAAAACATCTTCCCTTTGTTGCTGGAGCCATGATTCTCATACACGGCTGAGTA 715

RESULT 2  
AAC42068

DB 601 TGTCAAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGATTCTCATACAAACGGCTGAGTA 660  
QY 716 TTGGAATAGCAGGACTAGCGATCGCTGAAATAACAGATGOCACAAACTTATGTTGTTCA 775  
DB 661 TTGGAATAGCAGGACTAGCGATCGCTGAAATAACAGATGOCACAAACTTATGTTGTTCA 720  
QY 776 CCTGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGCAATGTCGCAAGAGAGTCTCT 835  
DB 721 CCTGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGCAATGTCGCAAGAGAGTCTCT 780  
QY 836 ACGGAACATATTCTGTAATCCCTTGGAGTACGGAGTGGAGTCTCTGTTTGCATAAT 895  
DB 781 ACGGAACATATTCTGTAATCCCTTGGAGTACGGAGTGGAGTCTCTGTTTGCATAAT 840  
QY 896 AAACAGTGTATCACGAGGAAAGGACAAAGACTTATTTCTTCAAGCATTTTATCAGGCTTT 955  
DB 841 AAACAGTGTATCACGAGGAAAGGACAAAGACTTATTTCTTCAAGCATTTTATCAGGCTTT 900  
QY 956 GCAGCTCATCCAAACACGAGAAACTTAAAGTGCCTAGATAACATGCTGTAGTTGTGGGAAG 1015  
DB 901 GCAGCTCATCCAAACACGAGAAACTTAAAGTGCCTAGATAACATGCTGTAGTTGTGGGAAG 960  
QY 1016 TGATGTTAATGCTCAGACCAATTTGAGACTCAGTTACGTTAGTGTGTTGAAGAACAC 1075  
DB 961 TGATGTTAATGCTCAGACCAATTTGAGACTCAGTTACGTTAGTGTGTTGAAGAACAC 1020  
QY 1076 GATTATGACCGTGTCCATTTTGTGAACAAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGC 1135  
DB 1021 GATTATGACCGTGTCCATTTTGTGAACAAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGC 1080  
QY 1136 AATTGATGTCTTGTTCAGAAATCTCAGGGCCGTGGAGAAATGCTTTGGAAGGATAACAAT 1195  
DB 1081 AATTGATGTCTTGTTCAGAAATCTCAGGGCCGTGGAGAAATGCTTTGGAAGGATAACAAT 1140  
QY 1196 TGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGTGTGGAGGGACCAACGGAGAT 1255  
DB 1141 TGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGTGTGGAGGGACCAACGGAGAT 1200  
QY 1256 CGTCTGGACGGCTCGACTGGCCCTTCTGTCATCTGCTGGAGAGGGCGTGGCGCCTCT 1315  
DB 1201 CGTCTGGACGGCTCGACTGGCCCTTCTGTCATCTGCTGGAGAGGGCGTGGCGCCTCT 1260  
QY 1316 TGCAAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAA 1375  
DB 1261 TGCAAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAA 1320  
QY 1376 GGGCTATGGCAGGGTGAAGGAAATGTTTCATGGAGCACCAATGGCTGAGAGGATCGCGGC 1435  
DB 1321 GGGCTATGGCAGGGTGAAGGAAATGTTTCATGGAGCACCAATGGCTGAGAGGATCGCGGC 1380  
QY 1436 GGTGTTGAAGGATGTCCTGAGGAAATCAAGAGCAGGAGCCTCCAGGTCTTGAGCTTTGCCGTG 1495  
DB 1381 GGTGTTGAAGGATGTCCTGAGGAAATCAAGAGCAGGAGCCTCCAGGTCTTGAGCTTTGCCGTG 1440  
QY 1496 CCCATCAGCTTGGCTAACATGTTGAACCTAGATTTTACGGGCTACGCCCTACGTTGTTTCA 1555  
DB 1441 CCCATCAGCTTGGCTAACATGTTGAACCTAGATTTTACGGGCTACGCCCTACGTTGTTTCA 1500  
QY 1556 GCTGTAAACTGTAGATTGGCACTCTGTTGGTCTACTTTTTCACATTCATGTTTACCTATT 1615  
DB 1501 GCTGTAAACTGTAGATTGGCACTCTGTTGGTCTACTTTTTCACATTCATGTTTACCTATT 1560  
QY 1616 AGCCATGTCCGATTCTATTCCAAATCATATAGGTTCTATTTCATCCATATAGATTAAAG 1675  
DB 1561 AGCCATGTCCGATTCTATTCCAAATCATATAGGTTCTATTTCATCCATATAGATTAAAG 1620  
QY 1676 AGGGATTGAGGAGATTTCATCTTAGT 1702  
DB 1621 AGGGATTGAGGAGATTTCATCTTAGT 1647

ID AAC42068 standard; DNA; 1715 BP.  
 XX  
 AC AAC42068;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34167.  
 XX  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway; metabolic pathway;  
 KW promoter; termination sequence; ss.  
 XX Arabidopsis thaliana.  
 PN EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-00301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825P.  
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PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 34.6%; Score 589.6; DB 3; Length 1715;  
Best Local Similarity 68.1%; Pred. No. 5e-156;  
Matches 818; Conservative 2; Mismatches 382; Indels 0; Gaps 0;

QY 266 GAGTCCCTCGGTTTCATGAGGTCCAAAGCTCGTGCCTCCTCGTCTCCCATGAGCTCTCCCT 325  
DB 351 GAATCCTCTAGATTTCATGAAATCGAAGCTCGTTTGTAGTATCCCAAGAGCTATCACT 410  
QY 326 CTCTGGTGGTCCACTTTTACTGATGGAATTAGCAATTTCTTCTGAGGCATGTTGGCTCGCA 385  
DB 411 CTCAVGTSGACCTTTGCTATTGATGGAATTGCGCTTTTGTTAAGAGGAGTTGGTCTGA 470  
QY 386 AGTGGTGTGGATAACAAACCAGAGATCACAGAAACAAATGATGTCACATATAGCTTGA 445  
DB 471 CGTTGTTTGGATCACTAATCAAAGCCACTTGAAGATGATGAAGTTGCTATAGTCTTGA 530  
QY 446 GCATAGGATGTTGAACCATGGAGTGCAGGTTTACCAGCTAGAGGACAGGAGGCTTGA 505

Db 531 ACACAAGATGTTGGATCGAGGAGTTCAGGTTATCTCTGCAAAGGTCAGAAAAGCTGTAGA 590  
QY 506 TATTGCTCTAAAAGCTGATCTGTTATCTTAAACACTGCTGTGCTGGCAAGTGGCTTGA 565  
Db 591 TACATCTCTCAAGGCTGATTTGATGTTCTTAAATACTGCTGGCTGGGAAATGGCTTGA 650  
QY 566 CCCTGTTCTGAAAGATCATGTTCTTAAAGTCTTCCGAAAGATTTTGTGGTGGATCCATGA 625  
Db 651 TGCTGTTCTAAAAGAAAATGTTGTTAAAGTTCTACCTAAGATCCTATGTTGGATTCATGA 710  
QY 626 AATGCGTGGCATTACTTTAAGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGC 685  
Db 711 GATGAGGAGACACTATTTCAATGCTGATTTGGTCAAAACACCTCCCTTTGTTGCAGGGC 770  
QY 686 CATGATTGATTCTCATACAAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCCTGAA 745  
Db 771 CATGATTGATTTCGATGCAACAGCTGGATACCTGGAATAACAGAACACAAAGCTCGCCTAGG 830  
QY 746 AATACAGATGCCACAAACTTATGTTGTTTACCTGGGGAATAGTAAAGAACTAATGGAAGT 805  
Db 831 GATTAAAATGCCAAAACTTACGTTGTGCACCTAGGAAATAGCAAGGAATGATGGAAGT 890  
QY 806 TGCTGAAGACAAATGTCGAAGAGAGTCTTACCTGGGAAACATAATTCGTGAATCCCTTGGAGT 865  
Db 891 AGCTGAAGATAGTGTGGCAAGAGAGTTCTCCGTGAGCACGTCGAGAAATCTCTTGGAGT 950  
QY 866 ACGGAGTGAGGATCTCCTGTTTGCATAATAAAACAGTGTATCAGGAGAAAGGACAAGA 925  
Db 951 GCGGAATGAAGACTTACTCTTTGGCATTATTAATAGTGTATCGCGTGGAAAGGCCAGGA 1010  
QY 926 CTTATTTCTTCAAGCATTTTATCAGGCTTTGCAGCTCATCCAACACGAGAAAACCTTAAAGT 985  
Db 1011 TCTGTTCTCCGAGCCTTCCACGAAAGTCTTGAAGAATCAAAGAGAAAGAACTTCAGGT 1070  
QY 986 GCCTAGAATACATGCTGTAGTTTGGGAAGTGTATGTTGCTGTTTTCAGAAATCTCAGGG 1045  
Db 1071 ACCAACAAATGCATGCAGTAGTAGTAGGAAGCGACATGAGCAAGCAGACAAAGTTCGAGAC 1130  
QY 1046 TCAGTTACGTGACTTTGTGGTGAAGAAACACGATTATGACCCGTTGTCATTTTGTGAACAA 1105  
Db 1131 AGAGCTACGCAACTTTGTCCGAGAAAAGAAACTTGAGAACTTTGTCCACTTCGTCAACAA 1190  
QY 1106 GACATTTGCGAGTGGCCCTTACTTTGGCAGCAATTTGATGTGCTTGTTCAGAAATCTCAGGG 1165  
Db 1191 AACTCTAACCGTAGCACCATATATAGCAGCCATAGACGTTCTTGTCCAAAACCTCCCAAGC 1250  
QY 1166 CCGTGGAGAAATGCTTTTGGAAAGGATAACAATTGAAGCAATGGCAATTCAGTTGCCAGTATT 1225  
Db 1251 CAGAGGAGAAATGCTTTGGGAGATAACAATCGAAGCCATGGCCTTTAAGCTACCTGTACT 1310  
QY 1226 GGGCACGGCTGCTGGAGGGACCAACGAGATCGTCTGGACGGCTCGACTGGCCTTCTGCA 1285  
Db 1311 TGGTACTGCAGCCGGAGGAACAATGGAGATTGTAGTGAATGGAACGACTGGTCTGTTACA 1370  
QY 1286 TCCTGCTGGGAAAGGAGGGCGTGGCGCTTCTTGCAAGAAACATCGTCAGACTCGCAAGCCA 1345  
Db 1371 TAGTGCAGGAAAGAGGAGTGATACCTCTCGCCAAGAACATAGTGAAGTTGGCGACGCA 1430  
QY 1346 CGCCGAGCAGAGGGTCTCCATGGGGGAAAAGGGCTATGGCAGGTTGAAGGAAATGTTTCAT 1405  
Db 1431 AGTTGAGTTACGGCTGAGAAATGGGAAAAAATGGGTATGAGAGAGTAAAAAGAGATGTTTTT 1490  
QY 1406 GGAGCACCATGGCTGAGAGGATCGCGGCGGTGTTGAAGGATGTTCTTGAGGAAATCACA 1465  
Db 1491 GGAACATCATATGTCAATCGAATAGCTTCGGTACTCAAAGAAAGTCTTGCAACACGCAAA 1550  
QY 1466 GG 1467  
Db 1551 GG 1552



ID ADR65394 standard; cDNA; 1094 BP.  
XX ADR65394;  
AC  
XX 02-DEC-2004 (first entry)  
DT  
XX Cotton cDNA sequence, SEQ ID 6175.  
DE  
XX Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;  
KW drought tolerance; plant disease resistance; galactomannan; lignin;  
KW plant growth regulator; heat tolerance; herbicide tolerance;  
KW homologous recombination; extreme osmotic condition tolerance;  
KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;  
KW stress resistance.  
XX  
OS Gossypium hirsutum.  
XX  
XX US2004181830-A1.  
PN  
XX 16-SEP-2004.  
PD  
XX 29-JAN-2004; 2004US-00767795.  
PF  
XX 07-MAY-2001; 2001US-00849529.  
PR  
XX 12-DEC-2001; 2001US-00021323.  
PR  
XX (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
XX  
PI Kovalic DK, Zhou Y, Cao Y;  
XX  
XX WPI; 2004-667718/65.  
DR  
XX New recombinant nucleic acid molecules and polypeptides from Gossypium  
PT hirsutum, useful for producing plants with improved biological  
PT characteristics (e.g. improved plant cold or drought tolerance).  
XX  
PS Claim 1; SEQ ID NO 6175; 14pp; English.  
XX  
XX The invention relates to a recombinant polynucleotide comprising any of  
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.  
CC Also a recombinant polypeptide comprising any of the 58798 amino acid  
CC sequences mentioned in the specification and producing a plant having an  
CC improved property. Producing a plant having an improved property  
CC comprises transforming a plant with a recombinant construct comprising a  
CC promoter region functional in a plant cell operably joined to a  
CC polynucleotide comprising a coding sequence for a polypeptide associated  
CC with the property, and growing the transformed plant. The polypeptide is  
CC useful for improving plant cold tolerance, manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, improving plant  
CC drought tolerance, providing increased resistance to plant disease,  
CC producing galactomannan (or lignin or plant growth regulators), improving  
CC plant heat tolerance, improving plant tolerance to herbicides, increasing  
CC the rate of homologous recombination in plants, improving plant tolerance  
CC to extreme osmotic conditions or to pathogens or pests, improving yield  
CC by modification of photosynthesis, modifying seed oil or protein yield  
CC and/or content, improving yield by modification of carbohydrate, nitrogen  
CC or phosphorus use and/or uptake, or improving yield by providing improved  
CC plant growth and development under at least one stress condition. The  
CC polynucleotide and polypeptide may also be used in recombinant DNA  
CC constructs, in physical arrays of molecules, as plant breeding markers,  
CC or in computer-based storage and analysis systems. The present sequence  
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585  
CC polynucleotide sequences were available, the remaining 52213  
CC polynucleotides and all 58798 protein sequences were not present.  
XX  
SQ Sequence 1094 BP; 335 A; 209 C; 258 G; 292 T; 0 U; 0 Other;  
Query Match 25.0%; Score 426.2; DB 13; Length 1094;

Best Local Similarity 65.0%; Pred. No. 9e-110;		Matches 666; Conservative 0; Mismatches 348; Indels 11; Gaps 2;	
Qy	627	ATGCGTGGGCATTACTTTAAGGTTGAATATGTCAACATCTTCCCTTTGTTGCTGGAGCC	686
Dd	13	ATGCGAGGCCATTTCTTTAAATTAGAGTATGTAAGCATGGAAGCTCTGTATCTGGTGCA	72
Qy	687	ATGATTGATTCTCATACACGGCTGAGTATTGGAATAGCA-----GGACTAGCGATCG	739
Dd	73	ATGATTGATTCAACAGCTCACAGCGGAATATTGGAAGATAACCCACGGCCGCCGCGCG	132
Qy	740	CCTGAAAATACAGATGCCACAACTTATGTTGTTTACCTGGGAATAGTAAAGAACTAAT	799
Dd	133	GCCGAAGATTAAATGCTGAGACCTATGTTGTTTACCTTGGAAATAGCAATGAACATGAT	192
Qy	800	GGAAAGTTGCTGAAGACAAATGTCGCAAGAGAGTCTTACGGGAACATATTCTGTAATCCCT	859
Dd	193	GCAAGTTGCAGAGACAGTGTGGCTAAAGGGTTTTTGGCTGAACATGTTCTGTAATCGCT	252
Qy	860	TGGAGTACGGAGTGAGGATCTCTGTTTGAATAATAAAGTGTATCACGAGGAAAGGG	919
Dd	253	TGGAGTGGCAATGACGATTTACTTCTTCCCTTAATAAATAGTGTTCACGAGGAAAGG	312
Qy	920	ACAAGACTTATTTCTTCAAGCATTTTATCAGGCTTTGCAAGTCTCATCCAACACGAGAACT	979
Dd	313	GCAGGATCTCTTCTACGCGCTTCTACGAGGCCCTTACAACTGATCAAGCAAAAGAAAT	372
Qy	980	TAAAGTGCCTAGAAATACATGCTGTAGTTGTGGGAAGTGTATTAATGCTCAGACCAATTT	1039
Dd	373	GCAGGTGCCACCATTTGCATGCAGTAATTGTGGGAAGTGCATGAGTGGCATACGAACT	432
Qy	1040	TGAGACTCAGTTACGTGACTTGTGTTGTTGAAGAACACAGATTCATGACCGTGTCCATTTGT	1099
Dd	433	TGAAATGGAATTACGAGCTTATGTAAACACAGAAATAATCAAGATCGTGTCTCACTTGT	492
Qy	1100	GAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATGATGTTGTTTCAAGAAATC	1159
Dd	493	GAACAAAACTCTAACAGTAGTCTCATATTTAGTGTCCGTAGATGTTCTTGTTCAGAAATC	552
Qy	1160	TCAGGCGCGTGGAGAAATGTTTGGGAAGGATAACAATTTGAAGCAATGGCATTTCAAGTTGCC	1219
Dd	553	TCAGGACGGGGAGAAATGTTTGGACGGATAACAATCGAAGCAATGGCATTTTCAGTTGCC	612
Qy	1220	AGT----ATTGGGCACGGCTGCTGGAGGGACCACCGAGAGTCTCTTGACGGCTCGACTG	1275
Dd	613	TGTCTGACAGGGAACAGCTCCGGGGGCACAAACGGAATAGTAGTGAACGGCACACAG	672
Qy	1276	GCCTTCTGCATCTCTGCTGGGAAGGAGGGCGTGGCGCTTTCGCAAGAAACATCGTCAGAC	1335
Dd	673	GTTTATTGCACCTCTGCTGGGAAGAGGGGTGACAACTTGGCGAAACATATTGTGAAC	732
Qy	1336	TCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAGGGCTATGGCAGGGTGAAG	1395
Dd	733	TAGCTACGCATGTAGAGAGGAGGCTTACAATAGGAAGAGAGGGGTACGAAAGGGTGAAG	792
Qy	1396	AAATGTTTCATGGAGCACCATGGCTGAGAGGATCGCGGGGTGTTGAAGGATGTCCTGA	1455
Dd	793	AAAGATTTCTAGAACATCACATGGCAGAGAGAAATGTTGTAAGTACTTAAAGAACGCTTGA	852
Qy	1456	GGAAATCACAGGAGCACTCCAGGTCTTGAGCTTTGCCGTGCCCATCAGCTTGGCTAACA	1515
Dd	853	GGAAGTCTAAATCAGATCAAGTAAACACCTTTGACAGTGAACACCCCGCCCATATAA	912
Qy	1516	TGTTGAAGTATTTTACGGGCTACGCCCTACGTTGTTTCCAGCTGTAAACTGTAGATTGCA	1575
Dd	913	AATTACAATGAGGTATATCCAGTTTCAATCAATATAATGAGTGAACATCTTTAATCTG	972
Qy	1576	CTGTTGGTCTACTTTTTTACATTCATGTTTTTACCTATTAGGCCATGTCCGATTTCTATT	1635
Dd	973	GCCTTTTCTTTTCTTCTCTGCTCTTCTTTTCAACTAGTTCGCGGTATGTAATATTATT	1032
Qy	1636	CCAAT 1640	

Db 1033 ACATT 1037

RESULT 4

ADS71019

ID ADS71019 standard; cDNA; 276 BP.

XX

AC ADS71019;

XX

DT 18-NOV-2004 (first entry)

XX

DE Corn seedling-derived polynucleotide (cpds), SEQ ID 6035.

XX

KW Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;

KW seed development; disease resistance; insect infestation; fungal disease;

KW bacterial infection; Goss' Bacterial Wilt; blight;

KW Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;

KW bacterial stripe; maize dwarf mosaic virus infection;

KW environmental stress; water stress; pH stress; temperature stress;

KW pollution; injury; pesticide.

XX

OS Zea mays.

XX

PN US2003237110-A9.

XX

PD 25-DEC-2003.

XX

PF 06-AUG-2001; 2001US-00923876.

XX

PR 12-MAY-1998; 98US-0085331P.

PR 21-APR-1999; 99US-00298329.

XX

XX (INCY-) INCYTE PHARM INC.

XX

PI Lalgudi RV, Ito LY, Sherman BK;

XX

DR WPI; 2002-195165/25.

XX

XX New corn seedling-derived polynucleotides and polypeptides, useful in

PT identifying and altering desired characteristics associated with growth

PT and development, disease resistance, environmental adaptability, quality

PT and yield.

XX

PS Claim 3; SEQ ID NO 6035; 33pp; English.

XX

CC The invention relates to a corn seedling-derived polynucleotide (cdp)

CC selected from ADS64985-ADS71316, or their complements and fragments. Also

CC included are a composition for the detection of altered expression of a

CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a

CC method of detecting a polynucleotide in a biological sample using a cdp,

CC a method for using oligomers (and amplification) to recover a regulatory

CC element from a DNA library using oligomers designed against a cdp, a

CC seedling specific regulatory element that regulates the expression of a

CC cdp, an expression vector containing a cdp or regulatory element, a plant

CC transformed with the vector, a host cell containing the vector (and

CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,

CC identifying a compound which binds a CDP and screening a plurality of

CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,

CC proteins, vectors, cells and antibodies are useful for the

CC identification, evaluation and alteration of seed growth and development,

CC disease resistance (e.g. to insect infestation, fungal disease, bacterial

CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus

CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf

CC mosaic virus infection) and resistance to environmental stress (e.g.

CC water stress, pH stress, temperature stress, pollution, injury or

CC pesticides. The present sequence is cdp cDNA sequence.

XX

SQ Sequence 276 BP; 64 A; 58 C; 83 G; 69 T; 0 U; 2 Other;

Query Match 15.4%; Score 262; DB 7; Length 276;

Best Local Similarity 99.3%; Pred. No. 1.6e-63;

Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1034 CAAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTTCATGACCGTGTCCA 1093

Db 1 CAAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTTCATGACCGTGTCCA 60

QY 1094 TTTTGTGAACAAGACATTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGTCTTGTTC 1153

Db 61 TTTTGTGAACAAGACATTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGTCTTGTTC 120

QY 1154 GAATTCCTCAGGGCCGTGGAGAAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTC 1213

Db 121 GAATTCCTCAGGGCCGTGGAGAAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTC 180

QY 1214 GTTGCAGTATTGGGCACGGCTGCTGGAGGGACCCACGGAGATCGTCTCGACGGCTCGAC 1273

Db 181 GTTGCAGTATTGGGCACGCTGCTGGAGGGACCCACGGAGATCGTCTCGACGGCTCGAC 240

QY 1274 TGGCCTTCTGCATCCTGCTGGGAAGGAGGGCGTGG 1308

Db 241 TGGCC-TCTGCATCCTGCTGGGAAGGAGGGCGTGG 274

RESULT 5

ADS71062

ID ADS71062 standard; cDNA; 257 BP.

XX

AC ADS71062;

XX

DT 18-NOV-2004 (first entry)

XX

DE Corn seedling-derived polynucleotide (cpds), SEQ ID 6078.

XX

KW Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;

KW seed development; disease resistance; insect infestation; fungal disease;

KW bacterial infection; Goss' Bacterial Wilt; blight;

KW Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;

KW bacterial stripe; maize dwarf mosaic virus infection;

KW environmental stress; water stress; pH stress; temperature stress;

KW pollution; injury; pesticide.

XX

OS Zea mays.

XX

PN US2003237110-A9.

XX

PD 25-DEC-2003.

XX

PF 06-AUG-2001; 2001US-00923876.

XX

PR 12-MAY-1998; 98US-0085331P.

PR 21-APR-1999; 99US-00298329.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Lalgudi RV, Ito LY, Sherman BK;

XX

DR WPI; 2002-195165/25.

XX

XX New corn seedling-derived polynucleotides and polypeptides, useful in

PT identifying and altering desired characteristics associated with growth

PT and development, disease resistance, environmental adaptability, quality

PT and yield.

XX

PS Claim 3; SEQ ID NO 6078; 33pp; English.

XX

CC The invention relates to a corn seedling-derived polynucleotide (cdp)

CC selected from ADS64985-ADS71316, or their complements and fragments. Also

CC included are a composition for the detection of altered expression of a

CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a

CC method of detecting a polynucleotide in a biological sample using a cdp,

CC a method for using oligomers (and amplification) to recover a regulatory

CC element from a DNA library using oligomers designed against a cdp, a

CC seedling specific regulatory element that regulates the expression of a

CC cdp, an expression vector containing a cdp or regulatory element, a plant

CC transformed with the vector, a host cell containing the vector (and



CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,  
CC identifying a compound which binds a CDP and screening a plurality of  
CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,  
CC proteins, vectors, cells and antibodies are useful for the  
CC identification, evaluation and alteration of seed growth and development,  
CC disease resistance (e.g. to insect infestation, fungal disease, bacterial  
CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial wilt, Helicoverpa  
CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf  
CC mosaic virus infection) and resistance to environmental stress (e.g.  
CC water stress, pH stress, temperature stress, pollution, injury or  
CC pesticides. The present sequence is cdp cDNA sequence.

SQ Sequence 257 BP; 61 A; 55 C; 73 G; 68 T; 0 U; 0 Other;

Query Match 15.1%; Score 257; DB 7; Length 257;

Best Local Similarity 100.0%; Pred. No. 4e-62;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 AAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCAT 1094

Db 1 AAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCAT 60

QY 1095 TTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATTGATGCTTTGTCAG 1154

Db 61 TTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATTGATGCTTTGTCAG 120

QY 1155 AATTCTCAGGCGCGTGGAGAAATGCTTTGGAAGGATAACAATTGAAGCAATGGCAATTCAG 1214

Db 121 AATTCTCAGGCGCGTGGAGAAATGCTTTGGAAGGATAACAATTGAAGCAATGGCAATTCAG 180

QY 1215 TTGCCAGTATTGGGCACGGCTGCTGGAGGACCACGGAGATCGTCTGGACGGCTCGACT 1274

Db 181 TTGCCAGTATTGGGCACGGCTGCTGGAGGACCACGGAGATCGTCTGGACGGCTCGACT 240

QY 1275 GGCCTTCTGCATCCTGC 1291

Db 241 GGCCTTCTGCATCCTGC 257

RESULT 6

ADR62845

ID ADR62845 standard; cDNA; 948 BP.

XX

AC ADR62845;

DT 02-DEC-2004 (first entry)

XX

DE Cotton cDNA sequence, SEQ ID 3626.

XX

KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;  
KW drought tolerance; plant disease resistance; galactomannan; lignin;  
KW plant growth regulator; heat tolerance; herbicide tolerance;  
KW homologous recombination; extreme osmotic condition tolerance;  
KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;  
KW stress resistance.

XX

OS Gossypium hirsutum.

XX

PN US2004181830-A1.

XX

PD 16-SEP-2004.

XX

PF 29-JAN-2004; 2004US-00767795.

XX

PR 07-MAY-2001; 2001US-00849529.

PR 12-DEC-2001; 2001US-00021323.

XX

PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.

PA (CAOY/) CAO Y.

XX

PI Kovalic DK, Zhou Y, Cao Y;

XX

DR WPI; 2004-667718/65.

XX New recombinant nucleic acid molecules and polypeptides from Gossypium  
PT hirsutum, useful for producing plants with improved biological  
PT characteristics (e.g. improved plant cold or drought tolerance).

XX Claim 1; SEQ ID NO 3626; 14pp; English.

XX The invention relates to a recombinant polynucleotide comprising any of  
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.  
CC Also a recombinant polypeptide comprising any of the 58798 amino acid  
CC sequences mentioned in the specification and producing a plant having an  
CC improved property. Producing a plant having an improved property  
CC comprises transforming a plant with a recombinant construct comprising a  
CC promoter region functional in a plant cell operably joined to a  
CC polynucleotide comprising a coding sequence for a polypeptide associated  
CC with the property, and growing the transformed plant. The polypeptide is  
CC useful for improving plant cold tolerance, manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, improving plant  
CC drought tolerance, providing increased resistance to plant disease,  
CC producing galactomannan (or lignin or plant growth regulators), increasing  
CC plant heat tolerance, improving plant tolerance to herbicides, increasing  
CC the rate of homologous recombination in plants, improving plant tolerance  
CC to extreme osmotic conditions or to pathogens or pests, improving yield  
CC by modification of photosynthesis, modifying seed oil or protein yield  
CC and/or content, improving yield by modification of carbohydrate, nitrogen  
CC or phosphorus use and/or uptake, or improving yield by providing improved  
CC plant growth and development under at least one stress condition. The  
CC polynucleotide and polypeptide may also be used in recombinant DNA  
CC constructs, in physical arrays of molecules, as plant breeding markers,  
CC or in computer-based storage and analysis systems. The present sequence  
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequences.html?DocID=20040181830. However only 6585  
CC polynucleotide sequences were available, the remaining 52213  
CC polynucleotides and all 58798 protein sequences were not present.

XX

SQ Sequence 948 BP; 242 A; 195 C; 220 G; 291 T; 0 U; 0 Other;

Query Match

Best Local Similarity 14.4%; Score 244.8; DB 13; Length 948;

Matches 352; Conservative 68.8%; Pred. No. 2.5e-58;

Mismatches 157; Indels 3; Gaps 1;

QY 249 ACCGCGTCGCCAGCGGAGTCCCTCGGGTTTCATGAGGTCCAGTCTCTCTCGTC 308

Db 393 ATCGCGGTGTGAAGCCGAGTCCGCTTAGCTTTATGAAGTCCAGCGTCCGCTGCTGTT 452

QY 309 TCCCATGAGCTCTCCCTCTCTGTTGGTCCACTTTTACTGATGAATTAGCATTTCTCTG 368

Db 453 TCGCAGCAGCTCTCGCTTCTGTTGGACCATTTGTTGCGATGGAGTGGCATTCCTATTA 512

QY 369 AGGCATGTTGGCTCGCAAGTGTGTGGATAACAACACAGAGATCACAGAACAATGAT 428

Db 513 AGAAGTGTGGTGTGAAGTTTATTGGATGACAATTATGAACCATCTGAAACAGATGAA 572

QY 429 GTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGGAGTTTACCAGCTAGA 488

Db 573 GTAACATATAGTTTAGAACATAAGATGTTGGACAGAGGATACAGGTATCTCAGCTAAG 632

QY 489 GGACAGGAGGAGTGTGATATTGCTCTTAAAGCTGATCTGGTTATCTTAAACACTGCTGTT 548

Db 633 GGGAAAGAAGCTTTAGATATCTGCTTAAGAGCTGATTTGGTTGTTTGAACACTGCTGTT 692

QY 549 GCTGGCAAGTGGCTTGACCCCTGTTCTGAAAGATCATGTTCTTAAAGTCTTCCGAAGATT 608

Db 693 GCTGGAAATGGCTGGATGTTGTTCTTAAGGGAGATGTTTCATCGTGTCTGCTTAAGGTTG 752

QY 609 TTGTGTTGGATCCATGAATGCGTGGGCGATTACTTTAAGGTTGATATGTCAACATCTT 668

Db 753 TTGTGTTGGATCCATGAATGCGTGGGCGATTACTTTAAGGTTGATATGTCAACATCTT 812

QY 669 CCCTTTGT---TGCTGGAGCCCATGATTGATTCTCATACAACGGCTGAGTATTGGAATAGC 725

Db 813 TCTCTTTTGTATCTGGTGCCTATGATTGATTCCTCATGTTTACAACAGAACTGGAAGAAT 872  
QY 726 AGGACTAGCGATCGCCTGAAATACAGATGCC 757  
Db 873 AGTACTAAAGAACGTTTGAAGTTTAAATGTC 904

RESULT 7  
ABX56781/c  
ID ABX56781 standard; DNA; 583 BP.  
XX  
AC ABX56781;  
XX  
DT 20-FEB-2003 (first entry)  
XX  
XX Arabidopsis thaliana polynucleotide #133.

DE Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;  
KW genetic modification; environmental stress; disease resistance;  
KW fungicide; insecticide; stress tolerance.

XX Arabidopsis thaliana.  
XX US2002040489-A1.  
PN  
XX  
PD 04-APR-2002.  
XX

PF 26-JAN-2001; 2001US-00770152.  
XX  
XX 27-JAN-2000; 2000US-0178503P.  
PR  
XX

PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.

XX Gorchach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
PI Hurban P;

XX WPI; 2003-110410/10.

XX Novel Arabidopsis thaliana nucleic acid useful for identifying homologous  
PT or related genes, and to create genetically modified and transgenic  
PT organisms, such as plant cells and plants.

XX Claim 1; SEQ ID NO 133; 45pp; English.

XX The invention relates to Arabidopsis thaliana nucleic acid sequences. The  
CC DNA sequences and the polypeptides they encode are useful for identifying  
CC homologous or related genes, for producing compositions that modulate the  
CC expression or function of the polypeptides, for mapping functional  
CC regions of the protein, in diagnosis, for studying associated  
CC physiological pathways, for genetic manipulation of cells, preferably  
CC plant cells, in screening assays of various plant strains to determine  
CC the strains that are capable of withstanding a particular disease or

CC environmental stress, for enhancing or inhibiting production of  
CC biosynthetic products in plants and to create genetically modified and  
CC transgenic organisms, such as plant cells and plants. Transgenic plants  
CC are useful for introducing or improving disease resistance and stress  
CC tolerance in plants, screening biologically active agents, such as  
CC fungicides and insecticides, and for elucidating biochemical pathways.  
CC Sequences ABX56649-ABX57647 represent Arabidopsis thaliana  
CC polynucleotides of the invention. Note: The sequence data for this patent  
CC did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 583 BP; 136 A; 141 C; 108 G; 198 T; 0 U; 0 Other;

Query Match 13.7%; Score 233; DB 10; Length 583;  
Best Local Similarity 66.3%; Pred. No. 4.2e-55;  
Matches 335; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 963 ATCCAACACGAGAACTTAAAGTCCTAGAAATACATGCTGTAGTTGTGGGAAGTGATGT 1022  
Db 568 ATCAAAGAGAAGAACTTCAGGTACCAACAATGCATGCATGTAGTAGGAGCGACATG 509  
QY 1023 AATGCTCAGACCACAAATTTGAGACTCAGTTACGTGACTTTTGGTGAAGAACACGATTTCAT 1082  
Db 508 AGCAAGCAGACAAAAGTTCGAGACAGAGCTACGCAACTTTGTCCGAGAAAAGAACTTGAG 449  
QY 1083 GACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATTGAT 1142  
Db 448 AACTTTTGTCCACTTCGTCAACAAAACCTCTAACCGTAGCACCATATATAGCAGCCATAGAC 389  
QY 1143 GTGCTTGTTCAGAAATTCACAGGCGGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCA 1202  
Db 388 GTTCTTTGTCCAAACTCCCAAGCCAGAGGAGATGCTTTGGGAGAATAACAATCGAAGCC 329  
QY 1203 ATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCCTG 1262  
Db 328 ATGGCCTTAAAGCTACCTGTACTTGGTACTGCAGCCGGAGGAACAATGGAGATTGTAGTG 269  
QY 1263 GACGGCTCGACTGGCCCTTCTGATCTCTGCTGGGAAGGAGGCGGTGGCCCTCTTGCAAAG 1322  
Db 268 AATGGAACGACTGGTCTGTACATAGTGCAGGGAAGAGAGTGATACCTCTCGCCAAG 209  
QY 1323 AACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAAGGGCTAT 1382  
Db 208 AACATAGTGAAGTTGGCGACGCAAGTTGAGTTACGGCTGAGAAATGGGAAAAATGGGTAT 149  
QY 1383 GGCAGGTGAAGGAAATGTTTCATGGAGCACCACATGGCTGAGAGGATCGCGGGTGTG 1442  
Db 148 GAGAGACTAAAAGAGATGTTTTTGGAAACATCATATGTCAATCGAATAGTTCGGTACTC 89  
QY 1443 AAGGATGTCTCTGAGGAAATCACAGG 1467  
Db 88 AAAGAAGTCTTGCAACACCGCAAAGG 64

RESULT 8

ADR62846

ID ADR62846 standard; cDNA; 625 BP.

XX

AC ADR62846;

XX

DT 02-DEC-2004 (first entry)

XX

DE Cotton cDNA sequence, SEQ ID 3627.

XX

KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;  
KW drought tolerance; plant disease resistance; galactomannan; lignin;  
KW plant growth regulator; heat tolerance; herbicide tolerance;  
KW homologous recombination; extreme osmotic condition tolerance;  
KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;  
KW stress resistance.

XX Gossypium hirsutum.

XX

PN US2004181830-A1.  
XX  
PD 16-SEP-2004.  
XX  
PF 29-JAN-2004; 2004US-00767795.  
XX  
PR 07-MAY-2001; 2001US-00849529.  
PR 12-DEC-2001; 2001US-00021323.  
XX  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
XX  
PI Kovalic DK, Zhou Y, Cao Y;  
XX  
XX WPI; 2004-667718/65.  
XX  
PT New recombinant nucleic acid molecules and polypeptides from Gossypium  
PT hirsutum, useful for producing plants with improved biological  
PT characteristics (e.g. improved plant cold or drought tolerance).  
XX  
PS Claim 1; SEQ ID NO 3627; 14pp; English.  
XX  
CC The invention relates to a recombinant polynucleotide comprising any of  
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.  
CC Also a recombinant polypeptide comprising any of the 58798 amino acid  
CC sequences mentioned in the specification and producing a plant having an  
CC improved property. Producing a plant having an improved property  
CC comprises transforming a plant with a recombinant construct comprising a  
CC promoter region functional in a plant cell operably joined to a  
CC polynucleotide comprising a coding sequence for a polypeptide associated  
CC with the property, and growing the transformed plant. The polypeptide is  
CC useful for improving plant cold tolerance, manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, improving plant  
CC drought tolerance, providing increased resistance to plant disease,  
CC producing galactonnan (or lignin or plant growth regulators), improving  
CC plant heat tolerance, improving plant tolerance to herbicides, increasing  
CC the rate of homologous recombination in plants, improving plant tolerance  
CC to extreme osmotic conditions or to pathogens or pests, improving yield  
CC by modification of photosynthesis, modifying seed oil or protein yield  
CC and/or content, improving yield by modification of carbohydrate, nitrogen  
CC or phosphorus use and/or uptake, or improving yield by providing improved  
CC plant growth and development under at least one stress condition. The  
CC polynucleotide and polypeptide may also be used in recombinant DNA  
CC constructs, in physical arrays of molecules, as plant breeding markers,  
CC or in computer-based storage and analysis systems. The present sequence  
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585  
CC polynucleotide sequences were available, the remaining 52213  
CC polynucleotides and all 58798 protein sequences were not present.  
SQ Sequence 625 BP; 144 A; 134 C; 158 G; 189 T; 0 U; 0 Other;  
Query Match 13.3%; Score 227; DB 13; Length 625;  
Best Local Similarity 70.7%; Pred. No. 2.2e-53;  
Matches 302; Conservative 0; Mismatches 125; Indels 0; Gaps 0;  
QY 240 GCCCTCAACACCGCGTCGCCAGCGGGAGTCCCTCGGGTTTCATGAGGTCCAAAGTCGTG 299  
Db 199 GCCCCGACATCGCTGCTGCAAGCGAGTCCACTCAGTTTCATGAAGTCCAAAGATTGTT 258  
QY 300 CTCCTGCTCCCATGAGCTCTCCCTCTCTGGTGGTCCACTTTTACTGATGGAATTAGCA 359  
Db 259 CTACTGGTGTGCACGAGCTCTCGCTTCTCTGGTGGACCATTTGTTGATGGAGTAGCA 318  
QY 360 TTTCTTCTGAGGCATGTTGGCTCGCAAGTGGTGTGGATAACAACACAGATCACAAGAA 419  
Db 319 TTTCTAATAAGAAGTGTGGTGTGCTGAAGTTAATTGGGTTACATTTATGAACCATCTGAA 378  
QY 420 ACAATGATGTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGTTTAA 479

Db 379 ACTGATGAAGTAATATATAGTTTAAACATAAGATGTTGGACAGAGGAGTGAGTTTTC 438  
QY 480 CCAGCTAGAGGACAGGAGGAGTGTGATATATTGCTCTAAAGCTGATCTGGTTATCTTAAAC 539  
Db 439 TCCGCGTTTGGAAAGAGCTATAGATACTGCTCTAAGAGCTGATTTGGTTGTTTGAAC 498  
QY 540 ACTGCTGTTGCTGGCAAGTGGTTCACCCCTGTTCTGAAAGATCATGTTCTTAAAGTCTCTT 599  
Db 499 ACAGCGTGTGCTGGGAAATGGGTAGATTATGTTCTTAAAGGAAGATATTACCGTGTCTG 558  
QY 600 CCGAAGATTTTGTGGTGGATCCATGAAATGCGTGGGCATTACTTTAAGGTTGAATATGTC 659  
Db 559 CCTAAGCTGTTGTGGTGGATCCATGAAATGCGAGGCCATTACTTCAAATTAGAGTATGTA 618  
QY 660 AAACATC 666  
Db 619 AAGCATC 625  
RESULT 9  
ACN58791  
ID ACN58791 standard; cDNA; 625 BP.  
XX  
AC ACN58791;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-012-Q6-K6-G10, SEQ:13572.  
XX  
KW Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoeceum;  
KW variety Nucotton33B; library LIB3829; molecular tag; molecular marker;  
KW genetic mapping; molecular mapping; seed germination; plant growth;  
KW plant quality; plant yield; plant breeding; tissue printing; ss.  
XX  
OS Gossypium hirsutum.  
XX  
PN US2004123340-A1.  
XX  
PD 24-JUN-2004.  
XX  
PF 12-DEC-2001; 2001US-00021323.  
XX  
PR 14-DEC-2000; 2000US-0255619P.  
XX  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
XX  
PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;  
XX  
XX WPI; 2004-479808/45.  
XX  
PT New isolated nucleic acid molecule that encodes a plant protein or its  
PT fragment, useful for isolating a variety of agronomically significant  
PT genes associated with plant growth, quality or yield, and as molecular  
PT tags to map genes.  
XX  
PS Claim 1; SEQ ID NO 13572; 34pp; English.  
XX  
CC The invention relates to 17880 cotton expressed sequence tags (ESTs;  
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated  
CC from primed or non-primed seeds from variety DP50B, mature seeds from  
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoeceum  
CC tissue, developing fibres, carpel walls and septa from variety  
CC Nucotton33B. The invention also relates to substantially purified  
CC proteins or their fragments encoded by nucleic acid molecules of the  
CC invention, and to transformed plants having a nucleic acid construct  
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as  
CC molecular tags to isolate genetic regions, to isolate genes, to map  
CC genes, to determine gene function and to determine whether genes are  
CC members of a particular gene family. The nucleic acid molecules may be  
CC used for isolating a variety of agronomically significant genes







QY 807 GCTGAAGACATGTCGCAAGAAGAGTCCTACGGGAACATATTCGTGAATCCCTTGGAGTA 866  
|||  
Db 193 GCAGAAGACAGTGGCTAAAGGGTTTTCGGTGAACATGTTTCGTGAATCGCTTGGAGTG 252  
|||  
QY 867 CGGAGTGAGGATCTCCTGTTTGCATATAATAAAGAGTGTATCAGGAGAAAGGACAAGAC 926  
|||  
Db 253 CGCAATGACGATTACTCTTTGCTTAAATAAGTGTATCAGGAGAAAGGACAGGAT 312  
|||  
QY 927 TTATTTCTCAAGCATTTTATCAGGCTTTCAGCTCATCCAAACAGGAGAAACTTAAAGTG 986  
|||  
Db 313 CTCTTTCTACGGCTTTTCTACGAGGCTTACAACTGATCAAGCAAAAGAAATGCAAGTG 372  
|||  
QY 987 CC 988  
|||  
Db 373 CC 374

RESULT 11  
ACN58833/c  
ID ACN58833 standard; cDNA; 514 BP.  
XX  
AC ACN58833;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-012-Q6-N6-G10, SEQ:13614.  
XX  
XX Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium;  
KW variety Nucotton33B; library LIB3829; molecular tag; molecular marker;  
KW genetic mapping; molecular mapping; seed germination; plant growth;  
KW plant quality; plant yield; plant breeding; tissue printing; ss.  
XX  
OS Gossypium hirsutum.  
XX  
PN US2004123340-A1.  
XX  
XX 24-JUN-2004.  
XX  
PF 12-DEC-2001; 2001US-00021323.  
XX  
PR 14-DEC-2000; 2000US-0255619P.  
XX  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
XX  
PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;  
XX  
DR WPI; 2004-479808/45.  
XX  
PT New isolated nucleic acid molecule that encodes a plant protein or its  
PT fragment, useful for isolating a variety of agronomically significant  
PT genes associated with plant growth, quality or yield, and as molecular  
PT tags to map genes.  
XX  
PS Claim 1; SEQ ID NO 13614; 34pp; English.  
XX  
XX The invention relates to 17880 cotton expressed sequence tags (ESTs;  
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated  
CC from primed or non-primed seeds from variety DP50B, mature seeds from  
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium  
CC tissue, developing fibres, carpel walls and septa from variety  
CC Nucotton33B. The invention also relates to substantially purified  
CC proteins or their fragments encoded by nucleic acid molecules of the  
CC invention, and to transformed plants having a nucleic acid construct  
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as  
CC molecular tags to isolate genetic regions, to isolate genes, to map  
CC genes, to determine gene function and to determining whether genes are  
CC members of a particular gene family. The nucleic acid molecules may be  
CC used for isolating a variety of agronomically significant genes  
CC associated with plant growth, quality, yield, and could also serve as

CC links in metabolic and catabolic pathways. The nucleic acid molecules are  
CC also useful for identifying genes important in initiating and maintaining  
CC seed germination or that may be used to mitigate stresses encountered  
CC during seed germination. The ESTs additionally enable the acquisition of  
CC promoters and cis-regulatory elements which will be useful to express  
CC agronomically significant genes in these tissues and/or other tissues,  
CC and also permits the acquisition of molecular markers useful in breeding  
CC schemes, genetic and molecular mapping, and in cloning of agronomically  
CC significant genes. The nucleic acid molecules are further useful for  
CC detecting the expression level or pattern of a protein or mRNA and for  
CC detecting the presence or quantity of a protein by tissue printing. The  
CC present sequence represents a specifically claimed EST isolated from a  
CC cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the US  
CC patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340  
XX  
SQ Sequence 514 BP; 136 A; 124 C; 90 G; 164 T; 0 U; 0 Other;  
  
Query Match 9.3%; Score 158.6; DB 13; Length 514;  
Best Local Similarity 70.4%; Pred. No. 5e-34;  
Matches 212; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
  
QY 1162 AGGGCCGTGGAGAAATGCTTTGGAGGATACCAATTGAAGCAATGGCATTCAGTTGCCAG 1221  
|||||  
Db 514 AGGACGGGGAGAAATGCTTTGGACGGATAACAATCGAAGCAATGGCATTCAGTTGCCCTG 455  
|||||  
QY 1222 TATTGGGCACGGCTGCTGGAGGGACCAACGAGATCGTCTGGACGGCTCGACTGGCCTTC 1281  
|||||  
Db 454 TGCTGGGAACAGCTGCCGGGGGACAAACGGAATAGTAGTGAACGGCACAAACAGGTTTAT 395  
|||||  
QY 1282 TGCACTCTGCTGGGAAGGAGGGCGTGGCGCCTCTTGTCAAAGAACATCGTCAGACTCGCAA 1341  
|||||  
Db 394 TGCACCTGCTGGGAAGAGGGGTGACAACACTCTGGCGAAACATATTGTGAAACTAGCTA 335  
|||||  
QY 1342 GCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAGGGCTATGGCAGGGTGAAGGAAATGT 1401  
|||||  
Db 334 CGCATGTAGAGAGGAGGCTTACATAGGAAGAGAGGGGTACGAAGGGTGAAGAAAGAT 275  
|||||  
QY 1402 TCATGGAGCACCACATGGCTGAGAGGATCGCGGGGCTGTTGAGGATGCTCTGAGGAAAT 1461  
|||||  
Db 274 TTCTAGAACATCATATGGCAGAGAGAAATGGTGAAGTACTTAAAGAACGTTGAGGAAGT 215  
|||||  
QY 1462 C 1462  
Db 214 C 214  
  
RESULT 12  
AAA311140  
ID AAA311140 standard; DNA; 284 BP.  
XX  
AC AAA311140;  
XX  
DT 05-JUL-2000 (first entry)  
XX  
DE Plant microsatellite marker #101.  
XX  
KW Plant microsatellite sequence; core repeat sequence; detection; probe;  
KW DNA polymorphism; genome mapping; physical mapping; fingerprinting;  
KW variety identification; genetic variability evaluation; primer; ss.  
OS Eucalyptus grandis.  
XX  
PN WO9967421-A1.  
XX  
PD 29-DEC-1999.  
XX  
PF 25-JUN-1999; 99WO-NZ000092.  
XX  
PR 25-JUN-1998; 98US-00105307.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.



RESULT 14  
ADA60128  
ID ADA60128 standard; cDNA; 254 BP.  
XX AC ADA60128;  
XX DT 20-NOV-2003 (first entry)  
XX DE Soybean sucrose synthase EST #28.  
XX KW Plant; ss; EST; expressed sequence tag; transgenic; sucrose pathway;  
KW triose phosphate isomerase; fructose 1, 6-bisphosphate aldolase;  
KW fructose 1, 6-bisphosphate; fructose 6-phosphate 2-kinase;  
KW phosphoglucose isomerase; vacuolar hydrogen translocating-pyrophosphatase;  
KW pyrophosphate-dependent fructose-6-phosphate phosphotransferase;  
KW invertase; sucrose synthase; hexokinase; fructokinase;  
KW nucleoside diphosphate kinase-kinase; NDP;  
KW glucose-6-phosphate 1-dehydrogenase; phosphoglucomutase; UDP;  
KW uridine diphosphate-glucose pyrophosphorylase; soybean.  
XX OS Glycine max.  
XX PN US2003135870-A1.  
XX PD 17-JUL-2003.  
XX PF 26-JAN-1999; 99US-00237183.  
XX PR 24-NOV-1997; 97US-0067000P.  
PR 09-DEC-1997; 97US-0069472P.  
PR 27-JAN-1998; 98US-0072888P.  
PR 10-FEB-1998; 98US-0074201P.  
PR 10-FEB-1998; 98US-0074280P.  
PR 10-FEB-1998; 98US-0074281P.  
PR 10-FEB-1998; 98US-0074282P.  
PR 12-FEB-1998; 98US-0074565P.  
PR 12-FEB-1998; 98US-0074566P.  
PR 12-FEB-1998; 98US-0074567P.  
PR 19-FEB-1998; 98US-0074789P.  
PR 19-FEB-1998; 98US-0075459P.  
PR 19-FEB-1998; 98US-0075460P.  
PR 19-FEB-1998; 98US-0075461P.  
PR 19-FEB-1998; 98US-0075462P.  
PR 19-FEB-1998; 98US-0075463P.  
PR 19-FEB-1998; 98US-0075464P.  
PR 06-MAR-1998; 98US-0076912P.  
PR 09-MAR-1998; 98US-0077229P.  
PR 09-MAR-1998; 98US-0077230P.  
PR 09-MAR-1998; 98US-0077231P.  
PR 18-MAR-1998; 98US-0078368P.  
PR 07-APR-1998; 98US-0080844P.  
PR 27-APR-1998; 98US-0083067P.  
PR 29-APR-1998; 98US-0083386P.  
PR 29-APR-1998; 98US-0083387P.  
PR 29-APR-1998; 98US-0083388P.  
PR 29-APR-1998; 98US-0083389P.  
PR 29-APR-1998; 98US-0083390P.  
PR 13-MAY-1998; 98US-0085222P.  
PR 13-MAY-1998; 98US-0085223P.  
PR 13-MAY-1998; 98US-0085224P.  
PR 21-MAY-1998; 98US-0086183P.  
PR 21-MAY-1998; 98US-0086184P.  
PR 21-MAY-1998; 98US-0086185P.  
PR 21-MAY-1998; 98US-0086186P.  
PR 21-MAY-1998; 98US-0086187P.  
PR 21-MAY-1998; 98US-0086188P.  
PR 01-JUN-1998; 98US-0087422P.  
PR 16-JUN-1998; 98US-0089524P.  
PR 18-JUN-1998; 98US-0089793P.  
PR 18-JUN-1998; 98US-0089810P.  
PR 18-JUN-1998; 98US-0089814P.  
PR 22-JUN-1998; 98US-0090170P.  
PR 26-JUN-1998; 98US-0090282P.  
PR 29-JUN-1998; 98US-0091035P.  
PR 30-JUN-1998; 98US-0091405P.  
PR 08-JUL-1998; 98US-0092036P.  
PR 09-SEP-1998; 98US-0099667P.  
PR 09-SEP-1998; 98US-0099670P.  
PR 09-SEP-1998; 98US-0099697P.  
PR 16-SEP-1998; 98US-0100672P.  
PR 16-SEP-1998; 98US-0100673P.  
PR 16-SEP-1998; 98US-0100674P.  
PR 21-SEP-1998; 98US-0101130P.  
PR 21-SEP-1998; 98US-0101131P.  
PR 21-SEP-1998; 98US-0101132P.  
PR 22-SEP-1998; 98US-0101343P.  
PR 22-SEP-1998; 98US-0101344P.  
PR 22-SEP-1998; 98US-0101347P.  
PR 22-SEP-1998; 98US-0101508P.  
PR 25-SEP-1998; 98US-0101707P.  
PR 13-OCT-1998; 98US-0104123P.  
PR 13-OCT-1998; 98US-0104124P.  
PR 13-OCT-1998; 98US-0104126P.  
PR 13-OCT-1998; 98US-0104127P.  
PR 13-OCT-1998; 98US-0104128P.  
PR 18-NOV-1998; 98US-0108996P.  
PR 19-NOV-1998; 98US-0109018P.  
PR 24-NOV-1998; 98US-00199129.  
PR 08-DEC-1998; 98US-00210297.  
PR 11-DEC-1998; 98US-0111981P.  
PR 22-DEC-1998; 98US-0113224P.  
PR 12-JAN-1999; 99US-00229413.  
XX  
PA (CHEI/) CHEIKH N.  
PA (FISH/) FISHER D K.  
PA (LIUJ/) LIU J.  
PI Cheikh N, Fisher DK, Liu J;  
XX WPI; 2003-688722/65.  
XX  
XX  
PT New maize or soybean enzymes and nucleic acid molecules associated with  
PT the sucrose pathway, useful for genome mapping, gene identification and  
PT analysis, plant breeding, or preparation of constructs for plant gene  
PT expression.  
PS Claim 2; Page; 117pp; English.  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC (appearing as ADA57847 - ADA60560 that encodes a maize or soybean enzyme  
CC or its fragment, associated with the sucrose pathway selected from:  
CC triose phosphate isomerase, fructose 1,6-bisphosphate aldolase, fructose  
CC 1,6-bisphosphate, fructose 6-phosphate 2-kinase, phosphoglucose isomerase,  
CC vacuolar hydrogen translocating-pyrophosphatase, pyrophosphate-dependent  
CC fructose-6-phosphate phosphotransferase, invertase, sucrose synthase,  
CC hexokinase, fructokinase, nucleoside diphosphate kinase (NDP)-kinase,  
CC glucose-6-phosphate 1-dehydrogenase, phosphoglucomutase and uridine .  
CC diphosphate (UDP)-glucose pyrophosphorylase. Also included are a  
CC substantially purified maize or soybean enzyme (or its fragment) and a  
CC transformed plant having a nucleic acid molecule. Also disclosed as new  
CC are purified antibodies capable of specifically binding to the maize or  
CC soybean enzyme, determining a level or pattern of a plant sucrose pathway  
CC enzyme in a plant cell or plant tissue, determining a mutation in a plant  
CC whose presence is predictive of a mutation affecting the level or pattern  
CC of a plant sucrose pathway enzyme, producing a plant containing an  
CC overexpressed or reduced level of plant sucrose pathway enzyme, reducing  
CC expression of a plant sucrose pathway enzyme in a plant and determining  
CC an association between a polymorphism and a plant trait. The maize or  
CC soybean enzymes and nucleic acid molecules are useful for genome mapping,  
CC gene identification and analysis, plant breeding, or preparation of  
CC constructs for plant gene expression and transgenic plants. The nucleic  
CC acid molecules are also useful as markers or probes. The present sequence  
CC is a soybean EST (expressed sequence tag) from a gene encoding a sucrose  
CC pathway enzyme. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format  
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.  
XX  
SQ Sequence 254 BP; 61 A; 53 C; 68 G; 69 T; 0 U; 3 Other;  
Query Match 4.0%; Score 67.4; DB 9; Length 254;  
Best Local Similarity 60.5%; Pred. No. 2.5e-08;  
Matches 127; Conservative 0; Mismatches 82; Indels 1; Gaps 1;  
QY 1116 GTGGCCCTTACTTGGCAGCAATTGATGTCTTGTTCAGAAATCTCAGGGCCGTGGAGAA 1175  
Db 11 GTTGCCTCACTTTACTCTGCCGCAGATGTTATGTTATAAACTCTCAGGGCTGGGAGAA 70  
QY 1176 TGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCT 1235  
Db 71 ACATTTGGACGTGTGACTATAGAGCAATGGCGTTTGGTCTTCGGTCTTGGGACGGAC 130  
QY 1236 GCTGAGGACCAACGAGATCGTCTTGACGGCTCGACTGGCCTTCTGCATCTCTGCTGG 1295  
Db 131 GCTGGAGGAACACAGGAGATTTGTTGAGCACAATGTTACAGGTC-TCTTCATCTGTTGGA 189  
QY 1296 AAGGAGGCGTGGCGCCTCTTGCAAGAAC 1325  
Db 190 CATCCGGGGAATCTTGTCTTGCANAGATC 219

RESULT 15  
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ID ADQ06025 standard; DNA; 254 BP.  
XX  
AC ADQ06025;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Soybean transcription factor seqid 2871.  
XX  
KW maize; soybean; Arabidopsis thaliana; transcription factor; homeobox;  
KW HLH; leucine zipper; zinc finger; transformed plant; plant;  
KW metabolic pathway; mutation detection; polymorphism; plant trait;  
KW genome mapping; gene identification; gene analysis; plant breeding;  
KW transgenic; ds.  
XX  
OS Glycine max.  
XX  
PN US2004123339-A1.  
XX  
PD 24-JUN-2004.  
XX  
PF 06-AUG-2001; 2001US-00922293.  
XX  
PR 24-NOV-1997; 97US-0067000P.  
PR 09-DEC-1997; 97US-0069472P.  
PR 13-JAN-1998; 98US-0071479P.  
PR 10-FEB-1998; 98US-0074201P.  
PR 10-FEB-1998; 98US-0074280P.  
PR 10-FEB-1998; 98US-0074281P.  
PR 10-FEB-1998; 98US-0074282P.  
PR 12-FEB-1998; 98US-0074565P.  
PR 12-FEB-1998; 98US-0074566P.  
PR 12-FEB-1998; 98US-0074567P.  
PR 19-FEB-1998; 98US-0074789P.  
PR 19-FEB-1998; 98US-0075459P.  
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PR 19-FEB-1998; 98US-0075464P.  
PR 09-MAR-1998; 98US-0077229P.  
PR 09-MAR-1998; 98US-0077230P.  
PR 09-MAR-1998; 98US-0077231P.  
PR 18-MAR-1998; 98US-0078368P.  
PR 07-APR-1998; 98US-0080844P.  
PR 27-APR-1998; 98US-0083067P.

PR 29-APR-1998; 98US-0083386P.  
PR 29-APR-1998; 98US-0083387P.  
PR 29-APR-1998; 98US-0083388P.  
PR 29-APR-1998; 98US-0083389P.  
PR 13-MAY-1998; 98US-0085222P.  
PR 13-MAY-1998; 98US-0085223P.  
PR 13-MAY-1998; 98US-0085224P.  
PR 15-MAY-1998; 98US-0085533P.  
PR 21-MAY-1998; 98US-0086183P.  
PR 21-MAY-1998; 98US-0086184P.  
PR 21-MAY-1998; 98US-0086185P.  
PR 21-MAY-1998; 98US-0086186P.  
PR 21-MAY-1998; 98US-0086187P.  
PR 21-MAY-1998; 98US-0086188P.  
PR 16-JUN-1998; 98US-0089524P.  
PR 18-JUN-1998; 98US-0089793P.  
PR 18-JUN-1998; 98US-0089806P.  
PR 18-JUN-1998; 98US-0089807P.  
PR 18-JUN-1998; 98US-0089808P.  
PR 18-JUN-1998; 98US-0089810P.  
PR 18-JUN-1998; 98US-0089811P.  
PR 18-JUN-1998; 98US-0089812P.  
PR 18-JUN-1998; 98US-0089813P.  
PR 18-JUN-1998; 98US-0089814P.  
PR 30-JUN-1998; 98US-0091247P.  
PR 30-JUN-1998; 98US-0091405P.  
PR 09-SEP-1998; 98US-0099667P.  
PR 09-SEP-1998; 98US-0099668P.  
PR 09-SEP-1998; 98US-0099670P.  
PR 09-SEP-1998; 98US-0099697P.  
PR 16-SEP-1998; 98US-0100672P.  
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PR 17-SEP-1998; 98US-0100963P.  
PR 21-SEP-1998; 98US-0101130P.  
PR 21-SEP-1998; 98US-0101131P.  
PR 21-SEP-1998; 98US-0101132P.  
PR 22-SEP-1998; 98US-0101343P.  
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PR 22-SEP-1998; 98US-0101347P.  
PR 22-SEP-1998; 98US-0101508P.  
PR 25-SEP-1998; 98US-0101707P.  
PR 13-OCT-1998; 98US-0104124P.  
PR 13-OCT-1998; 98US-0104126P.  
PR 13-OCT-1998; 98US-0104127P.  
PR 13-OCT-1998; 98US-0104128P.  
PR 18-NOV-1998; 98US-0108996P.  
PR 19-NOV-1998; 98US-0109018P.  
PR 24-NOV-1998; 98US-00199129.  
PR 08-DEC-1998; 98US-00210297.  
PR 11-DEC-1998; 98US-0111981P.  
PR 22-DEC-1998; 98US-0113224P.  
PR 12-JAN-1999; 99US-00229413.  
XX  
PA (CONN/) CONNER T W.  
PA (HECK/) HECK G R.  
PA (LIUJ/) LIU J.  
PI Conner TW, Heck GR, Liu J;  
XX  
DR WPI; 2004-468202/44.  
XX  
PT New substantially purified nucleic acid molecule that encodes a maize,  
PT soybean or Arabidopsis thaliana transcription factor or its fragment,  
PT useful for genome mapping, gene identification and analysis or plant  
PT breeding.  
XX  
PS Claim 2; SEQ ID NO 2871; 140pp; English.  
XX  
CC The invention describes a substantially purified nucleic acid molecule  
CC that encodes a maize, soybean or Arabidopsis thaliana transcription  
CC factor or its fragment, where the maize or soybean transcription factor  
CC is homeobox, HLH, leucine zipper, zinc finger, or other transcription



factor. Also described are: a substantially purified maize or soybean transcription factor or its fragment defined above; a substantially purified antibody or its fragment which is capable of specifically binding to the transcription factor or its fragment above; a transformed plant; a method for determining a level or pattern in a plant cell of a transcription factor in a plant metabolic pathway; a method of determining a mutation in a plant; a method of producing a plant containing an overexpressed protein ore reduced levels of plant transcription factor; a method of determining an association between a polymorphism and a plant trait; and a method of isolating a nucleic acid that encodes a plant transcription factor or its fragment. The nucleic acid molecules, proteins and their fragments are useful for genome mapping, gene identification and analysis, plant breeding, preparation of constructs for use in plant gene expression and transgenic plants. The nucleic acid molecules are useful as markers or probes. This sequence represents a soybeantranscription factor polynucleotide.

SQ Sequence 254 BP; 61 A; 53 C; 68 G; 69 T; 0 U; 3 Other;

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Query Match      4.0%;      Score 67.4;  DB 12;  Length 254;
Best Local Similarity 60.5%;  Pred. No. 2.5e-08;
Matches 127; Conservative 0; Mismatches 82; Indels 1; Gaps 1;
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QY 1236 GCTGGAGGGACCAAGAGATCGTCTCTGGACGGCTCGACTGGCCCTTCTGCATCCTGCTGGG 1295

Db 131 GCTGGAGGAACACAGGAGATTGTTGAGCACAATGTTACAGGTC-TCTTCATCTCTGTTGGA 189

QY 1296 AAGGAGGGCGTGGCGCTCTTGC AAGAAC 1325  
Db 190 CATCCGGGGAATCTTGTCTTGCANAGATC 219

Search completed: March 17, 2006, 00:14:58  
Job time : 1069 secs

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[illegible]

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RESULT 8
US-10-161-499-11
; Sequence 11, Application US/10161499
; Patent No. 6673354
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/161,499
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ndel-EcoR1
; OTHER INFORMATION: fragment
US-10-161-499-11

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Query Match	2.8%;	Score 48.2;	DB 3;	Length 912;
Best Local Similarity	47.2%;	Pred. No. 0.0054;		
Matches 146;	Conservative 0;	Mismatches 163;	Indels 0;	Gaps 0;
QY	3	TCGGCTCGAGTTTGATCCGAGCCACAGTCTCTCTCGGGCCACCGGTCGACCGGGCG 62		
Db	325	TCCGAGGGCCGACGACACCCACACACCGCCCCCGGGCCCCCGAAACCCAGCGGGTG 384		
QY	63	ATGGCAAAGACCCCGTGTTCGGGTGGCGCGGTGCGCGGAGSCGCGGGCCGGTTTCAC 122		
Db	385	CGACTAAGGCCCCCGGCCCCCGGGCGGAGACCAACCCGCGCAGGAAATCGGCCAG 444		
QY	123	AACCGGACCCAGTCT 182		
Db	445	CCAGAAATCCGCGGCACTCCCGAGACGCCCCCGCGTCCGACGGCGCCAAACCCGATCCAAGACA 504		
QY	183	GGGTTCTCTCTCCGCGGTGCCCTGCGAGACCTTTCGCGACGGCGGTGGGGACCCCGCCGCC 242		
Db	505	CCCGCGCAGGGGTGGCCAGAAAGTGCACTTTAGCACCCGCCCCCGCCAAACCCCGACGCG 564		
QY	243	CTCAACACCGCGTGCAGCGGGAGTCCCCTCGGGTTTCATGAGGTCCAAGCTCGTGCTC 302		

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Db      565  CCATGACCCCCCGGTGGCCGGCTTTAAACAAGCGGTCTTCTGCGCCGCGGTCTGGGCGC  624
QY      303  CTCGTCTCC 311
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        |||
Db      625  CTGGCGGCC 633

RESULT 9
US-09-230-421-1
; Sequence 1, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL AGENTS AND ASSAYS
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 950
; TYPE: DNA
; ORGANISM: HERPESVIRUS TYPE 1
US-09-230-421-1

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QY	303	CTCGTCTCC	311	
Db	666	CTGGCGGCC	674	

RESULT 10  
 US-09-937-837-1  
 ; Sequence 1, Application US/09937837  
 ; Patent No. 6773920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INVITROGEN CORPORATION  
 ; APPLICANT: DALBY, Brian  
 ; APPLICANT: BENNETT, Robert  
 ; TITLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN SEQUENCES  
 ; TITLE OF INVENTION: BY TRANSLOCATING POLYPEPTIDES  
 ; FILE REFERENCE: INVIT1280-1  
 ; CURRENT APPLICATION NUMBER: US/09/937,837  
 ; CURRENT FILING DATE: 2001-09-28  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08571  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR APPLICATION NUMBER: 60/127,467  
 ; PRIOR FILING DATE: 1999-03-31  
 ; NUMBER OF SEQ ID NOS: 21

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pVP22/Myc-His
US-09-937-837-1

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Query Match 2.8%; Score 48.2; DB 3; Length 6404;  
Best Local Similarity 47.2%; Pred. NO. 0.015;  
Matches 146; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

Qy	3	TCGGCTCGAGTTTGATCCGAGCCACAGTCTCTCTCGGGCCACCGCGTCCGACCGGGC	62
Db	1232	TCCGAGGGCGCGACGACACCCACCACCGCCCCCGGGCCCCCGAACCACGCGGTG	1291
Qy	63	ATGGCAAAGACCCCGTCGTTTCGGGTGGCGGTCGCGGAGGCCGCGGGCCGGTTCAC	122
Db	1292	GCGTCTAAGGCCCCCGGGCCCCCGGCGGAGACACCCGCGCAGGAATCGGCCACG	1351
Qy	123	AACCGGACCCAGCTCCTCTCTCTCTCGTGGCCGTCGAGCCTCCGCAATCCACAGCA	182
Db	1352	CCAGAATCCGCGGCACTCCAGACGCCCCCCCGCTCGACGGCGCAACCCGATCCAAGACA	1411
Qy	183	GGGTTCTCTCTCGCGGTGCCCTCGAGACCCCTTGGACGGCCCGTGGGGACCCCGCGCC	242
Db	1412	CCCGCGCAGGGGCTGGCCAGAAAGCTGCATTTAGCACCGCCCCCCCCAAACCCCGACGG	1471
Qy	243	CTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTTCATGAGGTCCAAGCTCGTGCTC	302
Db	1472	CCATGGACCCCCCGGTGGCCGGCTTTAAACAGCGCGTCTTCTGCGCCGCGGTGCGGCGC	1531
Qy	303	CTCGTCTCC	311
Db	1532	CTGGCGGCC	1540

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RESULT 11
US-09-937-837-2
; Sequence 2, Application US/09937837
; Patent No. 6773920
; GENERAL INFORMATION:
; APPLICANT: INVITROGEN CORPORATION
; APPLICANT: DALBY, Brian
; APPLICANT: BENNETT, Robert
; TITLE OF INVENTION: DELIVERY OF FUNCTIONAL PROTEIN SEQUENCES
; TITLE OF INVENTION: BY TRANSLOCATING POLYPEPTIDES
; FILE REFERENCE: INVT1280-1
; CURRENT APPLICATION NUMBER: US/09/937,837
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/US00/08571
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/127,467
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 6420
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vector pVP22/Myc-His-TOPO
US-09-937-837-2

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Query Match      2.8%; Score 48.2; DB 3; Length 6420;
Best Local Similarity 47.2%; Pred. No. 0.015;
Matches 146; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

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Qy 3 TC GGCTCGAGTTTGATCCGAGCCACAGTCTCTCTCGGGCCACCGCGTCCGACGGCG 62

Db 1232 TCCGAGGGGCCGACGCACACCCACACCGCCCCCGGGCCCCCGAACCCACGCGGTG 1291

QY	63	ATGGCAAAGACCCCGTTCGTTTCGGGTGGCGGCCGGTCTCGCGAGGC CGCGGCCGGTTCCAC	122
D <sub>b</sub>	1292	GCGACTTAAGGCCCCCGCGGCCCGCGGGAGACCACCCCGCGCAGAAATCGGCCCGAG	1351
QY	123	AACCGGACCCAGCTCCTCCTCCTCTCGTGCGCGCTCGCAGCCTCCGCATCCACAGCA	182
D <sub>b</sub>	1352	CCAGAATCCCGCGCAC TCC CAGACGCCCGCGCTCGACGGCGCCAACCCGATCCAAGACA	1411
QY	183	GGGTTCTCTCTCCGCGGTGCCCTCGGAGACCCCTTGCGACGGCCCGTGGGGACCCC CGCCGCC	242
D <sub>b</sub>	1412	CCCCGCGAGGGCTGGCCAGAAAGCTGCAC TT TAGCA CCGCCCCCCCCAACC CGACGCG	1471
QY	243	CTCAACACCCCGCTGCCAGCGGGAGTCCCCTCGGGTT CAT GAGGTCCAAGTCTCGTGCTC	302
D <sub>b</sub>	1472	CCATGGACCCCCCGGTGGCCGGCTTTAAC AAGCGCGTCTTCTGCGCCGCGGT CGGGCGC	1531
QY	303	CTCGTCTCC	311
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RESULT 12  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-F1s  
; US-08-232-463-14

Query Match 2.8%; Score 47.4; DB 2; Length 7218;  
Best Local Similarity 4.4%; Pred. No. 0.026;  
Matches 12; Conservative 160; Mismatches 101; Indels 0; Gaps 0;





Search completed: March 17, 2006, 04:44:36  
Job time : 334 secs

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QY 416 AGAAACAAATGATGTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGT 475  
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QY 476 TTTACCAGCTAGAGGACAGGAGGCAGTTGATATTGCTCTAAAAGCTGATCTGGTTATCTT 535  
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QY 536 AAACACTGCTGTTGCTGGCAAGTGGCTTGACCTGTTCTGAAAGATCATGTTCCATAAGT 595  
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QY 656 TGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGATCTCATACAACGGCTGAGTA 715  
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QY 716 TTGGAATAGCAGGACTAGCGATCGCTTGAAAAATACAGATGCCACAACTTATGTTGTTCA 775  
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QY 776 CCTGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGACAATGTCGAAGAAGAGTCTT 835  
Db 721 CCTGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGACAATGTCGAAGAAGAGTCTT 780  
QY 836 ACGGGAACATFATCGTGAATCCCTTGGAGTACGGAGTGAGGATCTCTGTTTGAATAAT 895  
Db 781 ACGGGAACATFATCGTGAATCCCTTGGAGTACGGAGTGAGGATCTCTGTTTGAATAAT 840  
QY 896 AAACAGTGATACAGGAGAAAGGACAAAGACTTATTCTTCAAGCAATTTATCAGGCTTT 955  
Db 841 AAACAGTGATACAGGAGAAAGGACAAAGACTTATTCTTCAAGCAATTTATCAGGCTTT 900  
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Db 901 GCAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGATAACATGCTGTAGTTGTGGGAAG 960  
QY 1016 TGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTTGTGGTGAAGAACAC 1075  
Db 961 TGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTTGTGGTGAAGAACAC 1020  
QY 1076 GATTCAATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGC 1135  
Db 1021 GATTCAATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTGGCAGC 1080  
QY 1136 AATTGATGTGTTTGTGAGAACTCTCAGGGCGGTGGAGAAATGCTTTGGAAGGATAACAAT 1195  
Db 1081 AATTGATGTGTTTGTGAGAACTCTCAGGGCGGTGGAGAAATGCTTTGGAAGGATAACAAT 1140  
QY 1196 TGAAGCAATGGCATTTCAAGTTGCCAGTATTGGSCACGGCTGCTGGAGGACCAAGGAGAT 1255  
Db 1141 TGAAGCAATGGCATTTCAAGTTGCCAGTATTGGSCACGGCTGCTGGAGGACCAAGGAGAT 1200  
QY 1256 CGTCTGGACGGCTCGACTGGCCTTCTGCTGCTGGAGAGGAGGCGTGGCGCCTCT 1315  
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QY 1316 TGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGTTCTCATTGGGGGAAAA 1375  
Db 1261 TGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGTTCTCATTGGGGGAAAA 1320  
QY 1376 GGGCTATGGCAGGTTGAAGGAAATGTTTCAATGAGACCAACATGGCTGAGAGGATCGCGGC 1435

Db 1321 GGGCTATGGCAGGTTGAAGGAAATGTTTATGGAGCACCATGGCTGAGAGGATCGCGGC 1380  
QY 1436 GGTGTTGAAGGATGTCTTGAGGAAATCACAGGAGCACTCCAGGTCTTGAGCTTTGCCGTG 1495  
Db 1381 GGTGTTGAAGGATGTCTTGAGGAAATCACAGGAGCACTCCAGGTCTTGAGCTTTGCCGTG 1440  
QY 1496 CCCATCAGCTTGGCTAACATGTTGAACTAGATTTTACGGGCTACGCCTACGTGGTTTCCAG 1555  
Db 1441 CCCATCAGCTTGGCTAACATGTTGAACTAGATTTTACGGGCTACGCCTACGTGGTTTCCAG 1500  
QY 1556 GCTGTAAACTGTAGATTGCACTCTGTTGGTCTACTTTTTTACATTTTACCTATT 1615  
Db 1501 GCTGTAAACTGTAGATTGCACTCTGTTGGTCTACTTTTTTACATTTTACCTATT 1560  
QY 1616 AGGCCATGTCGATTTCTATTCCAATTCATATAGGTTCTATTCAATCCATATAGATTAAG 1675  
Db 1561 AGGCCATGTCGATTTCTATTCCAATTCATATAGGTTCTATTCAATCCATATAGATTAAG 1620  
QY 1676 AGGGATTGAGGAGATTTCATCTTAGT 1702  
Db 1621 AGGGATTGAGGAGATTTCATCTTAGT 1647

RESULT 2

US-10-425-115-103279  
; Sequence 103279, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 103279  
; LENGTH: 1853  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_25696C.1  
US-10-425-115-103279

Query Match 93.5%; Score 1591.8; DB 8; Length 1853;  
Best Local Similarity 98.4%; Pred. No. 0;  
Matches 1631; Conservative 0; Mismatches 17; Indels 9; Gaps 2;

QY 1 ATTCGGCTCGAGTTTGATCCGAGCCACAGTCTCTCTCGGGCCACCGCGTCCGACCGG 60  
Db 1 ATTCGGCTCCCATTTGATCCGAGCCACAGTCTCTCTCGGGCCACCGCGTCCGACCGG 60  
QY 61 CGATGGCAAGACCCCGTTCGCGGTGGCGGTGCGCGAGGCGCGCGGCGCGGTTTC 120  
Db 61 CGATGGCAAGACCCCGTTCGCGGTGGCGGTGCGCGAGGCGCGGCGCGGTTTC 120  
QY 121 ACAACCGGACCCAGCT 180  
Db 121 ACAACCGGACCCAGCT 180  
QY 181 CAGGTTCT 240  
Db 181 CAGGTTCT 240  
QY 241 CCCTCAACACCGCCGTGCGCAGCGGAGTCCCTCTCGGTTTCATGAGGTCCAAAGTCTGTC 300  
Db 241 CCCTCAACACCGCCGTGCGCAGCGGAGTCCCTCTCGGTTTCATGAGGTCCAAAGTCTGTC 300  
QY 301 TCCTCGTCTCCCATGAGCT 360  
Db 301 TCCTCGTCTCCCATGAGCT 360





Db 361 ATAACAAACAGAGATCGAAGAAACAAATGATGTTACATATAGCTTGGAGCATAAGATG 420  
QY 456 TTGAACCATGGAGTGCAGGTTTTTACCAGCTAGAGGACAGGAGCGAGTTGATATTGCTCTA 515  
Db 421 TTGAGCCATGGAGTGCAGGTAATTACCTGTAGGGACATGAGGCGATTGATCTGCCCTA 480  
QY 516 AAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTG 575  
Db 481 AAGGCTGATCTTGTATCTTGAACACTGCTGTTGCTGGCAAGTGGCTTGATGCTGCCTA 540  
QY 576 AAAGATCATGTTCTTAAAGTCTTCCGAAGATTTTGTGGTGGATCCATGAAATGCGTGGG 635  
Db 541 AATGACCATGTTCCCAAGTCTTCCCAAGATTTTGTGGTGGATCCATGAAATGCGAGGG 600  
QY 636 CATTACTTTAAGGTTGAATATGTCAAACATCTTCCCTTTTGTGCTGGAGCCCATGATTGAT 695  
Db 601 CATTACTTTAAGCTTGAATATGTCAAACATCTTCCCTCTGTTGCTGGAGCCCATGATTGAT 660  
QY 696 TCTCATACACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCTGAAAAATACAGATG 755  
Db 661 TCTCATACACGGCTGAATATTGGAAGACAGGACTCATGACCGTTTGAANAATACAGATG 720  
QY 756 CCACAAACTTATGTTTTCACCTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGAC 815  
Db 721 CCACAAACTTATGTTTTCACCTCGGGAATAGTAAGGAGTTAATGGAAGTTGCTGAAGAT 780  
QY 816 AATGTCGCAAGAAGAGTCTTACGGGAACATATTTCGTGAATCCCTTGGAGTACGGAGTGAG 875  
Db 781 AATGTTGCAAGAAGAGTCTTACGGGAGCATATCCGTGAGTTCCCTGGAGTACGGAGTGAA 840  
QY 876 GATCTCCTGTTTGCAATAATAAACAAGTGTATCACGAGGAAAGGGACAAGACTTATTTCTT 935  
Db 841 GATCTTGTGTTGCAATAATAAACAAGTGTTCACGTGGAAAGGGCAGGACTTATTTCTT 900  
QY 936 CAAGCATTTTATCAGGCTTTGCGAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGAAATA 995  
Db 901 CAAGCGTTTTATCAGGGTGTCCAGCTCATCGAACAGAAAGATTAAAGTGCCCAACATG 960  
QY 996 CATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGT 1055  
Db 961 CATGCTGTAGTTGTGGGAAGTGACATAAATGCTCAGACCAAGTTTGAGACACAATTACGT 1020  
QY 1056 GACTTTGTGTGAAGAACACAGATTATGACCGTGTCCATTTTGTGAACAAGACATTGGCA 1115  
Db 1021 GATTTTGGCGTGAAGAAATGGGATTCAGGACCGGTTTCACTTTGTGAACAAGACATTAGCA 1080  
QY 1116 GTGGCCCTTACTTTGGCAGCAATTGATGTGCTTGTTCAGAAATTCCTCAGGCGCGTGAGAA 1175  
Db 1081 GTGGCTCCTTTATTTGGCTGCAACTGATGTGCTTGTTCAGAACTCTCAGGCGCGTGAGAA 1140  
QY 1176 TGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAGTTGCCAGTATTGGGCACGGCT 1235  
Db 1141 TGCTTTGGAAGGATAAACGATTGAAGCAATGGCATTCAGTTGCCAGTATTGGGCACGGCG 1200  
QY 1236 GCTGGAGGGACACGGAGATCGTCTGGACGGCTCGACTGGCCTTCTGCAATCCTGCTGGG 1295  
Db 1201 GCCGAGGGACACGGAGATCGTCTGGACGGCTCAACCGGCCTCTTGACCCCGCCGGG 1260  
QY 1296 AAGGAGGGCGTGGCGCCTCTTGCAAGAAACATCGTCAAGCTCGCAAGCCAGCCGAGCAG 1355  
Db 1261 AAGGAAGGCGTCGCGCCCTCGCGAAGAACATGTTAAGGCTCGCGAGGCCACGAAGAGGAC 1320  
QY 1356 AGGGTCTCCATGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGTTTCATGGAGCACCCAC 1415  
Db 1321 AGGGTCTCCATGGGTAGGAAAGGCTATGGCAGGGTGAAGGAAATGTTTCATGGAGCACCCAC 1380  
QY 1416 ATGGCTGAGAGGATCGCGCGGTTGTTGAAGGATGCTCTGAGGAAATCAAGAGGAGCACTCC 1475  
Db 1381 ATGGCTGGTAGGATCGCGGCCGTTGTTGCAGGAAGTTCTGAAGAAATCGCGGGAACATTCT 1440  
QY 1476 AGGTCTTGA 1484  
|||||

Db 1441 CACTCTTGA 1449  
RESULT 4  
US-10-767-701-12116  
; Sequence 12116, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 12116  
; LENGTH: 1048  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS10968\_1  
US-10-767-701-12116  
Query Match 45.6%; Score 776.4; DB 7; Length 1048;  
Best Local Similarity 95.7%; Pred. No. 4.4e-228;  
Matches 798; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 655 ATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGATTTCTCATACAACGGCTGAGT 714  
Db 1 ATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGATTTCTCATACAACGGCTGAAT 60  
QY 715 ATTGGAATAGCAGGACTAGCGATCGCCTGAAATACAGATGCCACAAACTTATGTTGTTTC 774  
Db 61 ATTGGAAGCAGGACTAGCGAGCCGCTAAATAACAGATGCCACAAACTTATGTTGTTTC 120  
QY 775 ACCTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGACAAATGTCGCAAGAGAGTCC 834  
Db 121 ACCTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGATAATGTCGCAAGAGAGTCC 180  
QY 835 TACGGGAACATATTTCGTGAATCCCTTGGAGTACGGAGTACGGAGTACCTCTGTTTGAATAA 894  
Db 181 TACGGGAACATATTTCGTGAATCCCTTGGAGTACGGAGTGAAGATCTCTGTTTGAATAA 240  
QY 895 TAAACAGTGTATCACGAGGAAAGGACAAAGACTTATTTCTTCAAGCAATTTATCAGGCTT 954  
Db 241 TAAACAGTGTATCACGAGGAAAGGACAAAGACTTATTTCTTCAAGCAATTTATCAGGCTT 300  
QY 955 TGCAGTCTCATCCAACACGAGAAACTTAAAGTGCCTAGAAATACATGCTGTAGTTGTGGAA 1014  
Db 301 TGCAGTCTCATCCAACACGAGAAACTTAAAGTGCCTACAATGCAATGCTATAGTTGTGGAA 360  
QY 1015 GTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACA 1074  
Db 361 GTGATATGAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAATG 420  
QY 1075 CGATTTCATGACCGTGTCCATTTTGTGAAACAAGACATTGGCAGTGGCCCTTACTTGGCAG 1134  
Db 421 CGATTTCATGACCGTGTCCATTTTGTGAAACAAGACATTGGCAGTGGCAGCTTATTTGGCAG 480  
QY 1135 CAATTGATGCTTGTTCAGAAATTTCAAGGCGCGTGGAGAAATGCTTTGGAAGGATAACAA 1194  
Db 481 CAATTGATGCTTGTTCAGAAATTTCCAGGCGCGTGGAGAAATGCTTTGGAAGGATAACAA 540  
QY 1195 TTGAAGCAATGGCATTCAAGTTGCCAGTATTTGGGCACGGCTGCTGGAGGACCCACGGAGA 1254  
Db 541 TTGAAGCAATGGCATTCAAGTTGCCAGTATTTGGGCACGGCTGCTGGAGGACCCACGGAAA 600  
QY 1255 TCGTCTCGAGCGGCTCGACTGGCCTTCTGCAATCCTGCTGGAAAGGAGGCGTGGCGCCTC 1314  
Db 601 TCGTCTCGAGCGGCTCGACTGGCCTTCTGCAATCCTGCTGGAAAGGAGGCGTGGACGCTC 660

QY	1315	TTGCAAGAAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGAAA	1374
Db	661	TTGCAAGAAACATTTGTGAGACTCGCAAGCCATGCCGAGCAAAAGGCTCTCCATGGGGAAA	720
QY	1375	AGGGCTATGGCAGGGTGAAGGAAATGTTTCATGGAGCACCAACATGGCTGAGAGGATCGCGG	1434
Db	721	AGGGCTATGACAGGGTGAAGGAAATGTTTCATGGAGCACCAACATGGCTGAGAGGATCGCGG	780
QY	1435	CGGTGTTGAAGGATGTCCTGAGGAAATCACAGGAGCACTCCAGGCTTTGAGCTT	1488
Db	781	CGGTGTTGAAGGAAAGTTCTGCGAAGAAATCACAGGAACCGCTTAGGCTTTGAGCTT	834

## RESULT 5

US-10-767-701-9892  
; Sequence 9892, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 9892  
; LENGTH: 667  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS39744\_1  
US-10-767-701-9892

Query Match	36.1%;	Score 614.2;	DB 7;	Length 667;
Best Local Similarity	95.1%;	Pred. No. 3.9e-178;		
Matches 634;	Conservative 0;	Mismatches 33;	Indels 0;	Gaps 0;
QY	17	ATCCGAGCCACAGTCTCTCCTCGGGCCACCGCGTCCGACCGCGGATGGCAAAGACCCC	76	
DB	1	ATCCGTGCTCACAGTCTCTCCTCGGGCCCGCGCTCGGCCCGCGATGGCGAAGCCCCC	60	
QY	77	GTCGTTCCGGTGGCGCGGTGCGCGGAGGCCCGGGCCGGTTCAACACCGGACCCAGCT	136	
DB	61	GTCGTCCGGCGGGCGGCCGCGCGGAGGCCCGGGCCGGTTCAACACCGGACCCGGCT	120	
QY	137	CCTCCTCCTCCTCTCGTGCCGTGCGCAGCCTCCGCATCCACAGAGGGTTCTCTCTCCG	196	
DB	121	CCTCCTCGTCTCTCTCGTGCCGTGCGCGCCTCCGCATCCACAGCGGGTTCTCTCTCCG	180	
QY	197	CGGTGCCCTGCGAGACCCCTTGCGACGGCCGTGGGACCCCGCCCTCAACACCCGCCGT	256	
DB	181	CGGTGCCCTGCGAGACCCCTGCGACGGCCGTGGAGACCCCGCCCTCAACACCCGCCGT	240	
QY	257	CGCCAGCGGGAGTCCCCCTCGGGTTTCATGAGGTCCAAGCTCGTGCTCTCTCGTCTCCCATGA	316	
DB	241	CGCCCGGGGAGTCCCCCTCGGGTTTCATGAGGTCCAAACTCGTGCTCTCTCGTCTCCACGA	300	
QY	317	GCTCTCCCTCTCTGGTGGTCCACTTTTACTGATGGAATTAGCATTTCTTCTGAGGCATGT	376	
DB	301	GCTCTCCCTTTTCGGGTGGCCCACTTTTACTGATGGAATTGGCATTTCTTCTGAGGCATGT	360	
QY	377	TGGCTCGCAAGTGGTGATGAACAAACAGAGATCAAGAAGAAATAATGATGTACATA	436	
DB	361	TGGTTCGGAAGTGGTGATGAACAAACAGAGATCAGAAGAAATAATGATGTACATA	420	
QY	437	TAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTTTACCAGCTAGAGGACAGGA	496	
DB	421	TAGCTTGGAGCATAGGATGTTGAGCCATGGAGTGCAGGTTTTTACCAGCTAGGGGACAGGA	480	
QY	497	GGCAGTTGATATTGCTCTAAAAGCTGATCTGGTTATCTTTAAACACTGCTGTTGCTGGCAA	556	

```

Db      481  GGCAGTTGATATTGCTCTCTAAAAGCTGATCTGGTTATCTTTAAACACTGCTGTTGTGGCAA 540
QY      557  GTGGCTTGACCCCTGTTCTGAAAGATCATGTTCTCTAAAGTCTTCCGAAGATTTTGTGGTG 616
Db      541  GTGGCTTGATCCTGTTCTGAAAGATCATGTTCTCTAAAGTCTTCCGAAGATTTTGTGGTG 600
QY      617  GATCCATGAAATGCGTGGGCATTACTTTAAAGTTGAATATGTCAAACATCTTCCCTTTGT 676
Db      601  GATCCATGAAATGCGAGGGCATTACTTTAAAGTTGAATATGTCAAACATCTTCCCTTTGT 660
QY      677  TGCTGGA 683
Db      661  TGCTGGA 667

RESULT 6
US-10-424-599-64438
; Sequence 64438, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 64438
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2395)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2919C.1
US-10-424-599-64438

```

## RESULT 6

US-10-424-599-64438  
; Sequence 64438, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 64438  
; LENGTH: 2395  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(2395)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_2919C.1  
US-10-424-599-64438

	Query Match	26.0%	Score 441.8;	DB 7;	Length 2395;
	Best Local Similarity	69.0%	Pred. No. 1.5e-124;		
	Matches 605;	Conservative 0;	Mismatches 272;	Indels 0;	Gaps 0;
QY	592	AAGTCCTCCGAAGATTTTGTGGTGGATCCATGAATGCGTGGGCATTACTTTAAGGTG	651		
Db	835	ATGGGCTTCGATGGGCTCGGTGGCTGCCCGGTGGCGTGGGCTTCTGCTCTGGCTGG	894		
QY	652	AATATGTCAAAACATCTTCCCTTTGTGTGGAGCCATGATTGATTCTCATACAACGGCTG	711		
Db	895	GATGTGGCTCGCTCCTCCCTTTGTGGCAGGGGCCGAGGGTCTCCCATACTGCTGCTG	954		
QY	712	AGTATTGGAATAGCAGGACTAGCGATCGCCTGAAAATACAGATGCCACAAACTTATGTTG	771		
Db	955	GGGGCTGCATGAATTGGCGGGCGTGCCTTGAGAGATTAAAAATGCCTGAAACTTTTGTG	1014		
QY	772	TTCACTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGACAATGTGCGCAAGAAGAG	831		
Db	1015	TACATCTTGGAAATAGCAGGAGCTTATGGAAGTTGCAGAAGATAGTGTGGCAAGAAGAG	1074		
QY	832	TCCTACGGGAACATATTCGTGAATCCCTTGGAGTACGGAGTGAGGATCTCCTGTTTGCAA	891		
Db	1075	TTCTTCGTGAGCATGTTTCGGGAATCTCTTGGAGTGGGCTCGAGTGATCTACTTTTTC	1134		
QY	892	TAATAAACAGTGTATCACGAGGAAGGGACAAGACTTATTTCTTCAAGCATTTTATCAGG	951		
Db	1135	TCATAAATAGTGTTCCTCGTGGTAAAGGGCAGGATCTATTTCTTCGCTCCTTTTATGAAA	1194		
QY	952	CTTTGCAGCTCATCCAAACACGAGAAAACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGG	1011		
Db	1195	GTTTGCAACTCATTACGAGGAAGAAAACCTCCAGTTGCCATTTTTCATGTGTGATAGTAG	1254		



QY	1012	GAAGTGATGTTAAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTGTGTGGAAGA	1071
DB	1255	GGAGTGATATGAATGCTCAGACAAAGTTTGAATGGAACTTCGCAAAATTTGTTGTTGAGA	1314
QY	1072	ACACGATTATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCCCTTACTTGG	1131
DB	1315	AAAAGATTCAGAATCGTGTTCACTTTGTTTAACAAAACCCCTGGCTGTGGCTCCTTACCTGG	1374
QY	1132	CAGCAATTGATGTGCTTGTTCAGAAATCTCAGGGCCGTGGAGAATGCTTTGGAAAGATAA	1191
DB	1375	CTGCTATTGATGTTCTTGTTCAAAATTTCTCAGGCACGGGAGAAATGTTTGGAAAGATAA	1434
QY	1192	CAATTGAAGCAATGGCAATTCAGTTGCCAGTATTTGGGCACGGCTGCTGGAGGGACCAACGG	1251
DB	1435	CCATTGAAGCAATGGCAATTCGGCTGCCCTGTACTGGGAACCTGCAGCTGGAGGCCACGATGG	1494
QY	1252	AGATCGTCTGGACGGCTCGACTGGCCCTTCTGCATCTCTGCTGGGAAGGAGGGCGTGGCGC	1311
DB	1495	AGATTGTGGTGAATGGGACAACCGGTTTGTCTGCATCTGTCTGGGAAAAGAGCGCTGACAC	1554
QY	1312	CTCTTGCAAAGAACATCGTTCAGACTCGCAAGCCAACGCCAGCAGAGGGTCTCCATGGGGG	1371
DB	1555	CTCTCGCCCAAGAACATGTGAAAATTGGCAAGTCATGTTGAGAAAGAGGCTTAACAATGGGAA	1614
QY	1372	AAAAGGGCTATGGCAGGGTGAAGGAAAATGTTTCATGGAGCACCAATGGCTGAGAGGATCG	1431
DB	1615	AGAAAGGGTATGAAGAAGTGAAGGAGAGATTTCTGGAGCCCCATATGTCGCAGAGAAATG	1674
QY	1432	CGCGGTGTTGAAGGATGTCTTGAGGAAAATCACAGGA	1468
DB	1675	CATTGGTTTTGAAGGAAGTTTTACAGAAGGCTTAAGCA	1711

## RESULT 7

US-10-767-795-6175  
; Sequence 6175, Application US/10767795  
; Publication No. US20040181830A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Zhou, Yihua  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53534)B  
; CURRENT APPLICATION NUMBER: US/10/767,795  
; CURRENT FILING DATE: 2004-01-30  
; NUMBER OF SEQ ID NOS: 117596  
; SEQ ID NO 6175  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C7042\_1  
US-10-767-795-6175

Query Match	25.0%;	Score 426.2;	DB 8;	Length 1094;
Best Local Similarity	65.0%;	Pred. No. 6.1e-120;		
Matches 666:	Conservative	0;	Mismatches 348;	Indels 11;
				Gaps 2;

Qy	627	ATGCGTGGGCATTACTTTAAGGTGAATATGTCAAAACATCTTCCCTTTGTGCTGGAGCC	686
Db	13	ATGCGAGGCCATTCTTTAAATTAGAGTATGTAAAGCATCGAACGTCTGTATCTGGTGCA	72
Qy	687	ATGATTGATTCTCATACAACGGCTGAGTATTGGAATAGCA-----GGACTAGCCGATCG	739
Db	73	ATGATTGATTACACCGTCAACGCGGAATATTGGAAGAAATACCCACGCGCGCGCGCG	132
Qy	740	CCTGAAAATACAGATGCCACAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACTAAT	799
Db	133	GCCGAAGATTAAATGCGCTGAGACCTATGTTGTTTCACCTTGGAAATAGCAATGAACTGAT	192
Qy	800	GGAAGTTGCTGAAGACAATGTGCGCAAGAAGAGTCCCTACGGGAACATATTCTGTAATCCCT	859

	D <sub>b</sub>	193	GCAAGTTGCAGAAGACAGTGTGGCTAAAAGGGTTTTTCGGTGAAACATGTTTCGTGAATCGCT	252
	Q <sub>y</sub>	860	TGGAGTACGGAGTGAGGATCTCCTGTTTGCAATAATAAACAGTGTATCACGAGGAAAGGG	919
	D <sub>b</sub>	253	TGGAGTGGCAATGACGATTACTCTTTGCCCTTAATAAATAGTGTTCACGAGGAAAAGG	312
	Q <sub>y</sub>	920	ACAAGACTTATTCTTCAAGCATTTTATCAGGCTTTGCAGCTCATCCAAACACGAGAAAACT	979
	D <sub>b</sub>	313	GCAGGATCTCTTTCTACGGCTTTCTACGAGGCCCTTACAAC TGATCAAGCAAAAAGAAAAAT	372
	Q <sub>y</sub>	980	TAAAGTGCTTAGAATACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACC AAAAT	1039
	D <sub>b</sub>	373	GCAGGTGCCACCATTTGCATGCAGTAATTGTGGGAAGTGACATGATGGCATACGAAACT	432
	Q <sub>y</sub>	1040	TGAGACTCAGTTACGTGACTTTTGTGGTGAAGAAACAGGATTCATGACCGCTGTCTCATTTTGT	1099
	D <sub>b</sub>	433	TGAAATGGAATTACGAGCTTATGTAAACAGAAAGAAAATTC AAGATCGTGTTCAC TTTTGT	492
	Q <sub>y</sub>	1100	GAACAAGACATTTGGCAGTGGCCCCCTTACTTTGGCAGCAATTGATGTGCTTGTTCAGAAATTC	1159
	D <sub>b</sub>	493	GAACAAAACCTTAACAGTAGCTCCATATTAGTGTCCGTAGATGTTCTTGTTCAGAAATTC	552
	Q <sub>y</sub>	1160	TCAGGGCCGTGGAGAAATGCTTTTGGAAAGGATAACAAATTGAAGCAATGGCATTTCAAGTTGCC	1219
	D <sub>b</sub>	553	TCAGGGACGGGGAGAAATGCTTTTGGACGGATACAAATCGAAGCAATGGCATTTTCAGTTGCC	612
	Q <sub>y</sub>	1220	AGT----ATTGGGCACGGCTGCTGGAGGGACCA CGGAGATCGTCTCTGGACGGCTCGACTG	1275
	D <sub>b</sub>	613	TGTGCTGACAGGGAAACAGCTGCCGGGGGCA CAACGGAAATAGTAGTGAACGGCAACAACAG	672
	Q <sub>y</sub>	1276	GCCTTCTGCATCTCTGGGAAGGAGGGCGTGGCGCTCTTGTGCAAAGAACATCGTTCAGAC	1335
	D <sub>b</sub>	673	GTTTATTGCACTCTGTGGAAAGAAAGGGGTGACAACTCTGGCGAAACATATTGTGAAAC	732
	Q <sub>y</sub>	1336	TCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGAAAGGGCTATGGCAGGGTGAAGG	1395
	D <sub>b</sub>	733	TAGCTACGATGTAGAGAGGAGGCTTACAATAGGAAAGAGAGGGGTACGAAAGGGTGAAAG	792
	Q <sub>y</sub>	1396	AAATGTTTCATGGAGCACCATGGCTGAGAGGATCGCGGGGTGTGTAAGGATGTCCTGA	1455
	D <sub>b</sub>	793	AAAGATTCTAGAACATCACATGGCAGAGAGAAATTGGTGAAGTACTTTAAGAAAGCGTTGA	852
	Q <sub>y</sub>	1456	GGAAATCAGGAGCACTCCAGGCTTTGAGCTTTGCCGTGCCCCATCAGCTTCGCGCTAACA	1515
	D <sub>b</sub>	853	GGAAGTCTAAAATCAGATCAAGTAAACACTTTGACAGTGAACACCCC GCGCCACCATAA	912
	Q <sub>y</sub>	1516	TGTTGAACTAGATTTTACGGGCTACGCCCTACGTGGTTCAGGCTGTAAACTGTAGATTGCA	1575
	D <sub>b</sub>	913	AATTACAATGAGGTATATCCAGTTTTC AATCAATATAATGGAGTGACATCTTTAAATTCG	972
	Q <sub>y</sub>	1576	CTCTGTGGTCTACTTTTTTTCACATTCATGTTTTTACCTATTAGGCCATGTCCGATTTCTATT	1635
	D <sub>b</sub>	973	GCCTTTTTTCTTTCTTCTCTCTCTCTCTTTTCAACTAGTTCGCCGTATGTAAATATTATT	1032
	Q <sub>y</sub>	1636	CCAAT	1640
	D <sub>b</sub>	1033	ACATT	1037

## RESULT 8

US-09-923-876-6035  
; Sequence 6035, Application US/09923876  
; Patent No. US20020013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Kamigaki, Laura Y. (Ito)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329



; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 6035
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458234H1
; NAME/KEY: unsure
; LOCATION: 200, 275
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-6035

Query Match
Best Local Similarity 15.4%; Score 262; DB 3; Length 276;
Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1034 CAAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCA 1093
Db 1 CAAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCA 60

Qy 1094 TTTTGTGAACAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGCTTGTTC 1153
Db 61 TTTTGTGAACAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGCTTGTTC 120

Qy 1154 GAATTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAA 1213
Db 121 GAATTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAA 180

Qy 1214 GTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCTGGACGGCTCGAC 1273
Db 181 GTTGCCAGTATTGGGCACGCTGCTGGAGGGACCACGGAGATCGTCTGGACGGCTCGAC 240

Qy 1274 TGGCCTTCTGCATCCTGCTGGGAAGGAGGGCGTGG 1308
Db 241 TGGCC-TCTGCATCCTGCTGGGAAGGAGGGCGTGG 274

RESULT 9
US-09-923-876-6035
; Sequence 6035, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 6035
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700458234H1
; NAME/KEY: unsure
; LOCATION: 200, 275
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-6035

Query Match
Best Local Similarity 15.4%; Score 262; DB 3; Length 276;
Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Best Local Similarity 99.3%; Pred. No. 1.3e-69;
Matches 273; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1034 CAAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCA 1093
Db 1 CAAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCA 60

Qy 1094 TTTTGTGAACAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGCTTGTTC 1153
Db 61 TTTTGTGAACAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGCTTGTTC 120

Qy 1154 GAATTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAA 1213
Db 121 GAATTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAA 180

Qy 1214 GTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCTGGACGGCTCGAC 1273
Db 181 GTTGCCAGTATTGGGCACGCTGCTGGAGGGACCACGGAGATCGTCTGGACGGCTCGAC 240

Qy 1274 TGGCCTTCTGCATCCTGCTGGGAAGGAGGGCGTGG 1308
Db 241 TGGCC-TCTGCATCCTGCTGGGAAGGAGGGCGTGG 274

RESULT 10
US-09-923-876-6078
; Sequence 6078, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 6078
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700458322H1
US-09-923-876-6078

Query Match
Best Local Similarity 15.1%; Score 257; DB 3; Length 257;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1035 AAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCAT 1094
Db 1 AAATTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCAT 60

Qy 1095 TTTGTGAACAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGCTTGTTCAG 1154
Db 61 TTTGTGAACAAGACATTTGGCAGTGGCCCCCTTACTTGGCAGCAATTGATGCTTGTTCAG 120

Qy 1155 AATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAA 1214
Db 121 AATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAA 180

Qy 1215 TTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCTGGACGGCTCGACT 1274
Db 181 TTGCCAGTATTGGGCACGCTGCTGGAGGGACCACGGAGATCGTCTGGACGGCTCGACT 240

Qy 1275 GGCCTTCTGCATCCTGC 1291

Db 241 GGCCTTCTGCATCCTGC 257

RESULT 11

US-09-923-876-6078

; Sequence 6078, Application US/09923876

; Publication No. US20030237110A9

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath V.

; APPLICANT: Kamigaki, Laura Y. (Ito)

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

; FILE REFERENCE: PL-0012-1 CON

; CURRENT APPLICATION NUMBER: US/09/923,876

; CURRENT FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: 09/298,329

; PRIOR FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: 60/085,331

; PRIOR FILING DATE: 1998-05-05

; NUMBER OF SEQ ID NOS: 6332

; SOFTWARE: PERL Program

; SEQ ID NO 6078

; LENGTH: 257

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20030237110A9 700458322H1

US-09-923-876-6078

Query Match 15.1%; Score 257; DB 3; Length 257;

Best Local Similarity 100.0%; Pred. No. 4.2e-68;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1035 AAATTGAGACTCAGTTACGTGACTTTGCGTGAAGAACACGATTCATGACCGGTGCCAT 1094

Db 1 AAATTGAGACTCAGTTACGTGACTTTGCGTGAAGAACACGATTCATGACCGGTGCCAT 60

QY 1095 TTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATTGATGTCTTGTTCAG 1154

Db 61 TTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAATTGATGTCTTGTTCAG 120

QY 1155 AATTCTCAGGCGCGTGGAGAAATGCTTTTGAAGGATAACAATTGAAGCAATGGCATTCAAG 1214

Db 121 AATTCTCAGGCGCGTGGAGAAATGCTTTTGAAGGATAACAATTGAAGCAATGGCATTCAAG 180

QY 1215 TTGCCAGTATTTGGCACGGCTGTCTGGAGGACCAACGGAGATCGTCTGGACGGCTCGACT 1274

Db 181 TTGCCAGTATTTGGCACGGCTGTCTGGAGGACCAACGGAGATCGTCTGGACGGCTCGACT 240

QY 1275 GGCCTTCTGCATCCTGC 1291

Db 241 GGCCTTCTGCATCCTGC 257

RESULT 12

US-10-767-795-3626

; Sequence 3626, Application US/10767795

; Publication No. US20040181830A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Cao, Yongwei

; APPLICANT: Zhou, Yihua

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53534)B

; CURRENT APPLICATION NUMBER: US/10/767,795

; CURRENT FILING DATE: 2004-01-30

; NUMBER OF SEQ ID NOS: 117596

; SEQ ID NO 3626

; LENGTH: 948

; TYPE: DNA

; ORGANISM: Gossypium hirsutum

; FEATURE:

; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C6051\_1

US-10-767-795-3626

Query Match 14.4%; Score 244.8; DB 8; Length 948;

Best Local Similarity 68.8%; Pred. No. 5.7e-64;

Matches 352; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

QY 249 ACCGCGTCGCCAGCGGGAGTCCCTCGGTTTCATGAGGTCCAAGCTCGTCTCCTCGTC 308

Db 393 ATCGCGCTGTGAAGCCGAGTCCGTTAGCTTTATGAAGTCCACGGTCCGCTGCTGTT 452

QY 309 TCCATGAGCTCTCCCTCTCTGGTGGTCCACTTTTACTGATGGAATTAGCATTTCTTCTG 368

Db 453 TCGCAGAGCTCTCGCTTCTCGTGGACCATTTGTTGGGATGGAGCTGGCATTCCTATTA 512

QY 369 AGGCATGTTGGCTCGCAAGTGGTGGATAACAACCAGAGATCAAGAACAATAATGAT 428

Db 513 AGAAGTGTGGTGTGAAGTTTATTTGGATGACAATTATGAACCATCTGAAACAGATGAA 572

QY 429 GTCACATATAGCTTGGAGCATAGGATTTGAACCATGGAGTGCAGGTTTACCAGCTAGA 488

Db 573 GTAACATATAGTTTAGAACATAGATGTTGGACAGAGGAGTACAGGTTATCTCAGCTAAG 632

QY 489 GGACAGGAGGCAGTTGATATTGCTCTAAAGCTGATCTGTTATCTTAAACACTGCTGTT 548

Db 633 GGGAAAGAAGCTTTAGATACCTGCTTAAGAGCTGATTTGGTGTGTTTGAACACTGCATTT 692

QY 549 GCTGGCAAGTGGCTTGACCCCTGTTCTGAAAGATCATGTTCTCTAAAGTCCCTCCGAAGATT 608

Db 693 GCTGGGAAATGGCTGGATGTTGTTCTTAAGGAGATGTTTCATCGTGTCTGCCTAAGGTG 752

QY 609 TTGTGTGGATCCATGAAATGCTGGGCACTTACTTTAAGGTTGAATATGTCAAACATCTT 668

Db 753 TTGTGTGGATCCATGAAATGCTGGGCACTTACTTTTAAATTAGACTATGTAAAGCATTTCT 812

QY 669 CCCTTTGT---TGCTGGAGCCATGATGATTTCTCATACAACGGCTGAGTATTGGAATAGC 725

Db 813 TCTCTTTTGTATCTGGTGCCTATGATTTGATTTCCCATGTTACACAGAATACTGGAAGAAT 872

QY 726 AGGACTAGCGATCGCCTGAAATAACAGATGCC 757

Db 873 AGTACTAAAGAACGTTTGAAGTTTAAATAATGTC 904

RESULT 13

US-09-770-152-133/c

; Sequence 133, Application US/09770152

; Publication No. US20020040489A1

; GENERAL INFORMATION:

; APPLICANT: Gorchach, Jörn

; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Kricker, Maja

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurban, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; FILE REFERENCE: 2025US (PARA-014PRV)

; CURRENT APPLICATION NUMBER: US/09/770,152



Db	259	CTACTGGTGTGCACGAGCTCTCGCTTCTGGTGGACCATTTGTTGTTGATGGAGCTAGCA	318
Qy	360	TTTCTTCTGAGGCATGTTGGCTCGCAAGTGGTGTGGATAACAACCAGAGATCACAAAGAA	419
Db	319	TTTTCTATTAAAGAGTGTGGTGTGAAGTTAATTGGGTTACATTTATGAACCACATCTGAA	378
Qy	420	ACAAATGATGTCACATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTTTA	479
Db	379	ACTGATGAAGTAATATATAGTTTAGACATAAGATGTTGGACAGAGAGTGCAGGTTTTTC	438
Qy	480	CCAGCTAGAGGACAGGAGGCAGTTGATATATTGCTCTAAAAGCTGATCTGTGGTTATCTTAAAC	539
Db	439	TCCGCGTTTGGAAAAAGAGCTATAGATACTGCTCTAAGAGCTGATTTGGTTGTTTGAAC	498
Qy	540	ACTGCTGTGCTGGCAAGTGGCTTGACCTGTTCTGAAAGATCATGTTCTTAAAGTCCTT	599
Db	499	ACAGCGGTGCTGGGAAATGGGTAGATTATGTTCTTAAAGGAAGATATTCACCGTGTCTG	558
Qy	600	CCGAAGATTTTGTGGTGATCCATGAATGCGTGGGCATTACTTTAAGGTTGAATATGTC	659
Db	559	CCTAAGGTGTTGTGGTGATCCATGAATGCGAGGCCATTACTTCAAATTAGAGTATGTA	618
Qy	660	AAACATC	666
Db	619	AAGCATC	625

Search completed: March 17, 2006, 05:35:53  
Job time : 1458 secs





Db 109394 CGCTCCCAAGGAGCGCCGGCCTCGCCCTCTCCGGCGTCCACGGCCGCGGC 109344

## RESULT 2

```

US-11-096-568A-19793
; Sequence 19793, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19793
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1621)
; OTHER INFORMATION: Ceres Seq. ID no. 12374562
US-11-096-568A-19793

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	Query Match	2.7%;	Score 46.6;	DB 9;	Length 1621;
	Best Local Similarity	49.8%;	Pred. No. 0.0092;		
Matches	118; Conservative	0;	Mismatches 119;	Indels	Gaps 0;
QY	92	GGCGGTGCGCGAGCCGGGCCGGTTTCAACAACGGACCAGACTCTCCTCCTCCTCCT	151		
Db	535	GGCGTAGCGCGCGCGGCCCTCGGACTCTGGCCTACTTCTTCCTGCTGGACGT	594		
QY	152	CGTGCGCGTTCGCAGCCTCCGCATCCACAGCAGGGTTCTCTCCTCCGCGGTGCCCTGCGAGA	211		
Db	595	GGCGGCCTTCGCGCTCGTCTGTCGCCGTCAAGCTCTTCGCCGTCGCGAGCCCCACCGCGT	654		
QY	212	CCCTTGCGACGGCCGTGGGACCCCGCCGCCCTCAACACCGCCGTCGCCAGCGGGAGTCC	271		
Db	655	CAAGTTCTTCGGCAGCGTCTGCCTCGCCTTCTCCATGGCCCGTCTTCGTGCGCCGCTCAG	714		
QY	272	CCTCGGGTTTCATGAGGTCCAAGCTCGTGTCTCCTCGTCTCCCATGAGCTCTCCCTCTC	328		
Db	715	CATCATCGTCAAGGTGGTCAAGACCAAGAGCGGTCCAGITTCCTTGCCCATCAGCCTCTC	771		

### RESULT 3

```

US-11-236-198-1
; Sequence 1, Application US/11236198
; Publication No. US20060030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70.US2.REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; CURRENT FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/668,558
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 23187
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
;
; NAME/KEY: misc feature
; LOCATION: 22324..23187
; OTHER INFORMATION: homology with USF2 gene in ref: embl Y07661
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 523..544
; OTHER INFORMATION: upstream amplification primer 17-2
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1047..1068
; OTHER INFORMATION: downstream amplification primer 17-2, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 946..963
; OTHER INFORMATION: upstream amplification primer 99-4576
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1385..1402
; OTHER INFORMATION: downstream amplification primer 99-4576, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1096..1115
; OTHER INFORMATION: upstream amplification primer 9-19
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1616..1635

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; OTHER INFORMATION: downstream amplification primer 9-19 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1602..1621
; OTHER INFORMATION: upstream amplification primer 9-20
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2074..2093
; OTHER INFORMATION: downstream amplification primer 9-20 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2036..2053
; OTHER INFORMATION: upstream amplification primer 99-4557
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2563..2580
; OTHER INFORMATION: downstream amplification primer 99-4557 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2084..2102
; OTHER INFORMATION: upstream amplification primer 9-1
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2483..2500
; OTHER INFORMATION: downstream amplification primer 9-1 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2470..2489
; OTHER INFORMATION: upstream amplification primer 9-21 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2062..2081
; OTHER INFORMATION: downstream amplification primer 9-21
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 3455..3474
; OTHER INFORMATION: upstream amplification primer 9-3
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 3882..3901
; OTHER INFORMATION: downstream amplification primer 9-3 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 3775..3792
; OTHER INFORMATION: upstream amplification primer 99-4558
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 4336..4356
; OTHER INFORMATION: downstream amplification primer 99-4558 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 4902..4920
; OTHER INFORMATION: upstream amplification primer 99-14419 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 4444..4463
; OTHER INFORMATION: downstream amplification primer 99-14419
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 6638..6655
; OTHER INFORMATION: upstream amplification primer 99-4577
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 7072..7089
; OTHER INFORMATION: downstream amplification primer 99-4577 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 7995..8012
; OTHER INFORMATION: upstream amplification primer 99-4559
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 8576..8593
; OTHER INFORMATION: downstream amplification primer 99-4559 , complement

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; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 9622..9639
; OTHER INFORMATION: upstream amplification primer 99-3148
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 10023..10040
; OTHER INFORMATION: downstream amplification primer 99-3148 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 9964..9981
; OTHER INFORMATION: upstream amplification primer 99-4560
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 10546..10563
; OTHER INFORMATION: downstream amplification primer 99-4560 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 10996..11015
; OTHER INFORMATION: upstream amplification primer 99-14411 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 10492..10512
; OTHER INFORMATION: downstream amplification primer 99-14411
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 11972..11990
; OTHER INFORMATION: upstream amplification primer 99-4561
; FEATURE:

Query Match      2.7%; Score 46.4; DB 9; Length 23187;
Best Local Similarity 48.7%; Pred. No. 0.043;
Matches 155; Conservative 0; Mismatches 161; Indels 2; Gaps 1;

Qy 35 TCCTCGGGCCACCGCGTCCGACCGGCGATGGCAAAGACCCCGTTCGCGGTGGCGGC 94
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21267 TCCCGGGGCACCGGAGTCCGGGGCCGGAGGAGAGACCCAGCCTGGCCCGCGCGC 21326

Qy 95 GGTCCGCGGAGGCGCGGGCGGTTTCAACACCGG--ACCAGGTCCTCCTCCTCCTC 152
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21327 CCGCGCGCGCGCGGAGAACGTGCCCCCGCAGCACCGCCGCGCTGCGTGGCGGCC 21386

Qy 153 GTGGCGGTGCGAGCCTCCGATCCACAGAGGTTCTCTCCGCGGTGCCGTGCGAGAC 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21387 GGCCCCCGCCAGGCGTGCATGCGCCGCGCCCGCCCTCCGCGCACCGCAGGTGGC 21446

Qy 213 CCTTGGACGGCGGTGGGACCCCGCGCCCTCAACACCGCGTCCGCGAGGAGTCCC 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21447 CGCGGGAGCGCGCGCGTCTCTCCCTTCCAGCCCATCCCCCGACCCCGCCACCG 21506

Qy 273 CTCGGGTTTCATGAGGTCCAAAGTCTGTCCTCTCTCCATGAGCTCTCCTCTCTGT 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21507 ACCTACTTTACTGTCTCCAAACTGGGCGAGCCACCTGGCCCCCGACGCCGCCCT 21566

Qy 333 GGTCCACTTTTACTGATG 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21567 GCTCCGGGTACCCCGACG 21584

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RESULT 4
US-11-096-568A-2921
; Sequence 2921, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 2921
; LENGTH: 1019

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Db 11 CG 10

RESULT 11

US-11-124-367A-5048/c  
; Sequence 5048, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124.367A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5048  
; LENGTH: 100000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-5048

Query Match 2.6%; Score 44; DB 12; Length 100000;  
Best Local Similarity 48.4%; Pred. No. 0.46;  
Matches 122; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 39 CGGGCCACCGCGTCCGACCGGCGATGCAAAAGACCCCGTCGTTCCGGTGGCGGCGTC 98  
Db 5889 CGGCTCCTCGCGCGGCTCCCGGCGCTCCCGCTCCCGCTCGGGCGCCCGGACGAGCG 5830  
QY 99 GCCGGAGGCGCGGCGCGGTTTCAACCGGACCCAGCTCCTCCTCCTCCTCGTGCC 158  
Db 5829 ACGGGAGGAGGAGCTGGGCGCGCGGAGCGGAAGCGCGCGCTTCCGCCCCCGCC 5770  
QY 159 GTCGAGCCTCCGCATCCACAGCAGGGTTCCTCCTCGCGGTGCTCCGCGAGACCTTGC 218  
Db 5769 GCCGCCACCGCGCCCCCGCACCGCGCGCGCTCCCGCGCGCGCGCGCGCGCG 5710  
QY 219 GACGGCGTGGGACCCCGCGCCCTCAACACCGCGCGTCCGCGAGGAGTCCCTCGGG 278  
Db 5709 GCGGCGCAGCG 5650  
QY 279 TTCATGAGGTCC 290  
Db 5649 CCCTGGAGGTGC 5638

RESULT 12

US-11-245-147-141  
; Sequence 141, Application US/11245147  
; Publication No. US20060030541A1  
; GENERAL INFORMATION:  
; APPLICANT: GARCIA, TERESA  
; APPLICANT: ROMAN ROMAN, SERGIO  
; APPLICANT: BARON, ROLAND  
; APPLICANT: CALL, KATHERINE  
; APPLICANT: THEILHABER, JOACHIM  
; APPLICANT: CONNOLLY, TIMOTHY  
; APPLICANT: JACKSON, AMANDA  
; APPLICANT: BUSHNELL, STEVEN  
; APPLICANT: RAWADI, GEORGES  
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE  
; FILE REFERENCE: 37991-0023  
; CURRENT APPLICATION NUMBER: US/11/245,147  
; CURRENT FILING DATE: 2005-10-07

; PRIOR APPLICATION NUMBER: PCT/IB02/02211  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/281,400  
; PRIOR FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 141  
; LENGTH: 2187  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-245-147-141

Query Match 2.6%; Score 43.8; DB 9; Length 2187;  
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Matches 123; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 69 AAGACCCCGTCTGTCGGGTGGCGGCGGTGCGCGAGGCGCGGCGCGGTTCACAAACCGG 128  
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QY 129 ACCAGCTCCTCCTCCTCCTCCTCGTGGCGCGTCCGAGCGCTCCGATCCACAGGAGTTC 188  
Db 919 CACGACCAACAGTCCCGCACATGTCGCCCAACCGCGGTTCACCTACATGGCCAGTGC 978  
QY 189 CTCTCCGCGGTGCGGTCGCGAGACCTTCGACGCGCGCGTGGGACCCCGCGCTCAAC 248  
Db 979 CCGGTGCGCGGGACCCCGGGCGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1038  
QY 249 ACCGCGTCCGCGCGCGGAGTCCCTCGGTTTCATGAGGTCCAGCTCGTCTCGTCTC 308  
Db 1039 GGGCGGACAGCAGCAGCGCGGTACCTCGTCCCGCGCATGGCGAGCGCGCATCGAA 1098  
QY 309 TCCCATGAGCTCTCC 323  
Db 1099 TGCCACTCGCCCTAC 1113

RESULT 13

US-10-016-686-14  
; Sequence 14, Application US/10016686  
; Publication No. US20060014222A1  
; GENERAL INFORMATION:  
; APPLICANT: Oxford Biomedica (UK) Limited  
; APPLICANT: Kingsman, Alan  
; APPLICANT: Kingsman, Susan Mary  
; APPLICANT: Bebbington, Christopher Robert  
; APPLICANT: Carrol, Miles William  
; APPLICANT: Ellard, Fiona Margaret  
; APPLICANT: Myers, Kevin Alan  
; TITLE OF INVENTION: Antibodies  
; FILE REFERENCE: 674523-2012  
; CURRENT APPLICATION NUMBER: US/10/016,686  
; CURRENT FILING DATE: 2002-11-02  
; PRIOR APPLICATION NUMBER: PCT/GB00/04317  
; PRIOR FILING DATE: 2000-11-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 1263  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: canine 5T4 polypeptide having the amino acid sequence  
US-10-016-686-14

Query Match 2.6%; Score 43.6; DB 7; Length 1263;  
Best Local Similarity 52.2%; Pred. No. 0.06;  
Matches 121; Conservative 0; Mismatches 109; Indels 2; Gaps 1;

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LOCUS AY107383 843 bp mRNA linear HTC 24-FEB-2005  
DEFINITION Zea mays PC0096987 mRNA sequence.  
ACCESSION AY107383  
VERSION AY107383.1 GI:21210461  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays  
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clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 843)  
REFERENCE  
AUTHORS Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H.,  
Fang,Z., Morgante,M., Landewe,T., Fengler,K., Useche,F.,  
Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H.  
Jr.

TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the  
bacterial artificial chromosome contig map by two-dimensional  
overgo hybridization  
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)  
PUBMED 15020742  
REFERENCE 2 (bases 1 to 843)  
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,  
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of  
Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 3 (bases 1 to 843)  
AUTHORS Coe,E.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
Missouri, Columbia, MO 65211, USA  
COMMENT If you are interested in getting corresponding physical clones,  
these are publicly available from ZmDB and may be found by BLAST  
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
Schnable, Iowa State, then clones may be requested from ZmDB:  
www.zmdb.iastate.edu.  
FEATURES  
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contigs to seed DuPont contigs; this resource was  
assembled by DuPont as part of a collaboration for the  
overgo addressing of BACs in conjunction with the Maize  
Mapping Project"  
ORIGIN  
Query Match 47.9%; Score 815.4; DB 4; Length 843;  
Best Local Similarity 99.2%; Pred. No. 6.le-219;  
Matches 827; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
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Qy 139 TCCT 198  
Db 130 TCCT 189  
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Qy 259 CCAGCGGAGTCCCCTCGGGTTTCATGAGGTCCAAGCTCGTCTCTCTCTCTCTCTCTCTCT 318  
Db 250 CCAGCGGAGTCCCCTCGGGTTTCATGAGGTCCAAGCTCGTCTCTCTCTCTCTCTCTCT 309  
Qy 319 TCTCCCT 378  
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Qy 439 GCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTTTACCAGTAGAGGACAGGAGG 498



Db 430 GCTTGGAGCATAGGATGTTGAACCATGAGTGCAGGTTTTTACCAGCTAGAGGACAGGAGG 489

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Db 550 GGCTTGACCTGTTCTGAAAGATCATGTTCTCTAAAGTCCTTCCGAAGATTTTGTGGTGA 609

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Qy 679 CTGGAGCCATGATTGATTTCTATACACGGCTGAGTATTGGAATAGCAGGACTAGCGATC 738

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RESULT 4

DR802416

LOCUS DR802416 758 bp mRNA linear EST 27-JUL-2005

DEFINITION ZM\_BFb0026K16.r ZM\_BFb Zea mays cdNA 5', mRNA sequence.

ACCESSION DR802416

VERSION DR802416.1 GI:71331165

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 758)

AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE Maize Full-length cDNA Project

JOURNAL Unpublished (2005)

COMMENT Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0026 row: K column: 16.

FEATURES

source

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/cultivar="B73"

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/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM\_BFb"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for

selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 44.3%; Score 753.8; DB 8; Length 758; Best Local Similarity 99.6%; Pred. No. 1.6e-201; Matches 755; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 30 GTCTCTCTCGGGCCACCGCGTCCGACCGGCGGATGGCAAGACCCCGTTCGCGGTG 89

Db 1 GTCCCTCTCGGGCCACCGCGTCCGACCGGCGGATGGCAAGACCCCGTTCGCGGTG 60

Qy 90 GCGGCGGTGCGCGGAGGCGCGGCGGGTTCACAACCGGACCCAGCTCCTCCTCCTC 149

Db 61 GCGGCGGTGCGCGGAGGCGCGGCGGGTTCACAACCGGACCCAGCTCCTCCTCCTC 120

Qy 150 CTCGTGGCGGTGCGAGCCTCCGATCCACAGCAGGGTTCCTCCTCCGCGGTGCCCTGCGA 209

Db 121 CTCGTGGCGGTGCGAGCCTCCGATCCACAGCAGGGTTCCTCCTCCGCGGTGCCCTGCGA 180

Qy 210 GACCTTTCGACGGCGGTGGGACCCCGCGCCCTCAACACCGCGTCCGACGCGGAGT 269

Db 181 GACCTTTCGACGGCGGTGGGACCCCGCGCCCTCAACACCGCGTCCGACGCGGAGT 240

Qy 270 CCCCTCGGGTTCATGAGGTCCAAGCTCGTCTCCTCGTCTCCATGAGCTCTCCCTCTCT 329

Db 241 CCCCTCGGGTTCATGAGGTCCAAGCTCGTCTCCTCGTCTCCATGAGCTCTCCCTCTCT 300

Qy 330 GGTGTCCACTTTTACTGATGGAATTAGCATTTCTTCTGAGGCATGTTGGTCGCAAGTG 389

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Qy 390 GTGTGATAACAAACAGAGATCAAGAAGAAACAAATGATGTCAATATAGCTTGGAGCAT 449

Db 361 GTGTGATAACAAACAGAGATCAAGAAGAAACAAATGATGTCAATATAGCTTGGAGCAT 420

Qy 450 AGGATGTTGAACCATGGAGTGCAGGTTTACAGCTAGAGGACAGGAGGCAGTTGATATT 509

Db 421 AGGATGTTGAACCATGGAGTGCAGGTTTACAGCTAGAGGACAGGAGGCAGTTGATATT 480

Qy 510 GCTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCT 569

Db 481 GCTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCT 540

Qy 570 GTTCTGAAAAGATCATGTTCTCTAAAGTCTTCCGAAGATTTTGTGTGGATCCATGAAATG 629

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Qy 630 CGTGGCATTACTTTAAGTTGAATATGTCAAAACATCTTCCCTTTGTTGCTGGAGCCATG 689

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Qy 750 CAGATGCCACAAAATTATGTTGTTTACCTGGGGAATAG 787

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DEFINITION ZM_BFb0009H19.f ZM_BFb Zea mays cDNA 3', mRNA linear EST 27-JUL-2005
ACCESSION DR790488
VERSION DR790488.1 GI:71308499
KEYWORDS
SOURCE
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 752)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE Maize Full-length cDNA Project
JOURNAL Unpublished (2005)
COMMENT Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0009 row: H column: 19.
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/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.3e-201;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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632 TTGTGGGAAGTGATGTTAATGCTCAGACCACAAATTTGAGACTCAGTTACGTGACTTTGTGG 573
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Db
32 TTTACCTATTAGGCCATGTCGATTCATTCTATTC 1
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DEFINITION ZM_BFb0030M17.r ZM_BFb Zea mays cDNA 5', mRNA linear EST 28-JUL-2005
ACCESSION DR805336
VERSION DR805336.1 GI:71421195
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 732)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE Maize Full-length cDNA Project
JOURNAL Unpublished (2005)
COMMENT Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
```

Email: yeisoo@genome.arizona.edu  
Plate: 0030 row: M column: 17.

FEATURES

Source

Location/Qualifiers  
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/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM\_BFb"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

ORIGIN

Query Match 43.0%; Score 732; DB 8; Length 732;  
Best Local Similarity 100.0%; Pred. No. 2.4e-195;  
Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	37	CTCGGGCCACCGCTCCGACCGCGATGSCAAAGACCCCGTCGTTCCGGTGGCGGG	96
Db	1	CTCGGGCCACCGCTCCGACCGCGATGSCAAAGACCCCGTCGTTCCGGTGGCGGG	60
QY	97	TCGCCGAGGCGCGGGCGGTTCAACAACCGGACCCAGCTCCTCCTCCTCCTCCTCGTGG	156
Db	61	TCGCCGAGGCGCGGGCGGTTCAACAACCGGACCCAGCTCCTCCTCCTCCTCCTCGTGG	120
QY	157	CCGTCGCAGCCTCCGCATCCACAGAGGGTTCTCCTCCGCGGTGCCCTGCGAGACCCCTT	216
Db	121	CCGTCGCAGCCTCCGCATCCACAGAGGGTTCTCCTCCGCGGTGCCCTGCGAGACCCCTT	180
QY	217	GCGACGGCCGTGGGACCCCGCCGCTCAACACCGCCGTCGCCAGCGGAGTCCCTCG	276
Db	181	GCGACGGCCGTGGGACCCCGCCGCTCAACACCGCCGTCGCCAGCGGAGTCCCTCG	240
QY	277	GTTTCATGAGTCCAAAGCTCGTCTCCTCGTCTCCCATGAGCTCCTCCTCCTCGTGGTC	336
Db	241	GTTTCATGAGTCCAAAGCTCGTCTCCTCGTCTCCCATGAGCTCCTCCTCCTCGTGGTC	300
QY	337	CACCTTTACTGATGGAATTAGCATTTCTCTGAGGCATGTTGGCTCGCAAGTGGTGGA	396
Db	301	CACCTTTACTGATGGAATTAGCATTTCTCTGAGGCATGTTGGCTCGCAAGTGGTGGA	360
QY	397	TAAACAAACGAGATCACAAGAAACAAATGATGTACATATAGCTTGGAGCATAGGATGT	456
Db	361	TAAACAAACGAGATCACAAGAAACAAATGATGTACATATAGCTTGGAGCATAGGATGT	420

QY	457	TGAACCATGGAGTGCAGGTTTACACAGCTAGAGGACAGGAGCAGTTGATATTGCTCTAA	516
Db	421	TGAACCATGGAGTGCAGGTTTACACAGCTAGAGGACAGGAGCAGTTGATATTGCTCTAA	480
QY	517	AAGCTGATCTGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTGA	576
Db	481	AAGCTGATCTGTTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCCTGTTCTGA	540
QY	577	AAGATCATGTTCTTAAAGTCTTCCGAAGATTTTGTGTTGGATCCCATGAAATGCGTGGGC	636
Db	541	AAGATCATGTTCTTAAAGTCTTCCGAAGATTTTGTGTTGGATCCCATGAAATGCGTGGGC	600
QY	637	ATTACTTTAAGGTTGAATATGTCAAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGATT	696
Db	601	ATTACTTTAAGGTTGAATATGTCAAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGATT	660
QY	697	CTCATACAAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCTGAAAATACAGATGC	756
Db	661	CTCATACAAACGGCTGAGTATTGGAATAGCAGGACTAGCGATCGCTGAAAATACAGATGC	720
QY	757	CACAAACTTATG 768	
Db	721	CACAAACTTATG 732	

RESULT 7

DR802415/c  
LOCUS  
DEFINITION  
ZM\_BFb0026K16.f ZM\_BFb Zea mays cDNA 3', mRNA sequence.  
ACCESSION  
DR802415  
VERSION  
DR802415.1 GI:71331163  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 730)

REFERENCE  
AUTHORS

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,  
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
Maize Full-length cDNA Project  
Unpublished (2005)

TITLE  
JOURNAL  
COMMENT

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The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
Plate: 0026 row: K column: 16.  
Location/Qualifiers  
1. .730  
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/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM\_BFb"

FEATURES

Source

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 42.9%; Score 730; DB 8; Length 730;  
Best Local Similarity 100.0%; Pred. No. 8.8e-195;  
Matches 730; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	886	TTGCAATAATAACAGTGTATCACGAGAAAGGGACAAGACTTATTTCTTCAAGCATTTT	945
Db	730	TTGCAATAATAACAGTGTATCACGAGAAAGGGACAAGACTTATTTCTTCAAGCATTTT	671
Qy	946	ATCAGGCTTTGCAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAG	1005
Db	670	ATCAGGCTTTGCAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAG	611
Qy	1006	TTGTGGGAAGTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTGTGG	1065
Db	610	TTGTGGGAAGTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGACTTTGTGG	551
Qy	1066	TGAAGAACACGATTTCATGACCGTGTCATTTTGTGAACAAGACATTTGGCAGTGGCCCTT	1125
Db	550	TGAAGAACACGATTTCATGACCGTGTCATTTTGTGAACAAGACATTTGGCAGTGGCCCTT	491
Qy	1126	ACTTGGCAGCAATTGATGTGCTTGTTCAGAAATCTCAGGGCCGTGGAGAATGCTTTGGAA	1185
Db	490	ACTTGGCAGCAATTGATGTGCTTGTTCAGAAATCTCAGGGCCGTGGAGAATGCTTTGGAA	431
Qy	1186	GGATAACAATTGAAGCAATGGCAATTCAGTTGCCAGTATTGGGCAGGCTGCTGGAGGGA	1245
Db	430	GGATAACAATTGAAGCAATGGCAATTCAGTTGCCAGTATTGGGCAGGCTGCTGGAGGGA	371
Qy	1246	CCACGGAGATCGTCTGGACGGCTCGACTGGCCCTTCTGCATCCTGCTGGGAAGGAGGCG	1305
Db	370	CCACGGAGATCGTCTGGACGGCTCGACTGGCCCTTCTGCATCCTGCTGGGAAGGAGGCG	311
Qy	1306	TGGCGCCTTTGCAAGAACAATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGCTCTCCA	1365
Db	310	TGGCGCCTTTGCAAGAACAATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGCTCTCCA	251
Qy	1366	TGGGGGAAAGGGCTATGGCAGGGTGAAGAAATGTTTCATGGAGCACCACATGGCTGAGA	1425
Db	250	TGGGGGAAAGGGCTATGGCAGGGTGAAGAAATGTTTCATGGAGCACCACATGGCTGAGA	191
Qy	1426	GGATCGGGCGGTGTTGAAGGATGCTCTGAGGAAATCACAGGACACTCCAGGTCTTGAG	1485
Db	190	GGATCGGGCGGTGTTGAAGGATGCTCTGAGGAAATCACAGGACACTCCAGGTCTTGAG	131
Qy	1486	CTTTGCCGTGCCCATCAGCTTGCCTAAACATGTTGAACATAGATTTACGGGCTACGCCTA	1545
Db	130	CTTTGCCGTGCCCATCAGCTTGCCTAAACATGTTGAACATAGATTTACGGGCTACGCCTA	71
Qy	1546	CGTGGTTCAGGCTGTAAACTGTAGATTGCACCTCTGTTGGTCTACTTTTTCACATTTCATGT	1605
Db	70	CGTGGTTCAGGCTGTAAACTGTAGATTGCACCTCTGTTGGTCTACTTTTTCACATTTCATGT	11
Qy	1606	TTTACCTATT	1615
Db	10	TTTACCTATT	1

RESULT 8

DR790489  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

DR790489 715 bp mRNA linear EST 27-JUL-2005  
ZM\_BFb0009H19.r ZM\_BFb Zea mays cDNA 5', mRNA sequence.  
DR790489  
DR790489.1 GI:71308501  
EST.  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 715)  
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
Maize Full-length cDNA Project  
Unpublished (2005)  
Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
Plate: 0009 row: H column: 19.  
Location/Qualifiers  
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/organism="Zea mays"  
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/cultivar="B73"  
/db\_xref="taxon:4577"  
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/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM\_BFb"  
/note="Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match	41.0%;	Score 698.2;	DB 8;	Length 715;
Best Local Similarity	99.4%;	Pred. No. 8.9e-186;		
Matches 711;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
Qy	37	CTCGGGCCACCGCGTCCGACCGGCGATGGCAAAGACCCCGTCGTTGGCGTGGCGCGG	96	
Db	1	CTCGGGCCACCGCGTCCGACCGGCGATGGCAAAGACCCCGTCGTTGGCGTGGCGCGG	60	
Qy	97	TCGCGGAGCGCGCGGGCGGGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCGTGG	156	







KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.

REFERENCE 1 (bases 1 to 879)  
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
TITLE The libraries that made SUCEST  
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
COMMENT Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 093 row: D column: 01  
Seq primer: T7 Promoter Primer.  
Location/Qualifiers  
1. .879  
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/mol\_type="mRNA"  
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/lab\_host="DH10B"  
/clone\_lib="ST3"  
/note="Organ: Fourth apical internodes of adult  
plants; Vector: pSport1; Site\_1: SalI; Site\_2: NotI; An  
unidirectional cDNA library generated from [Fourth apical  
stalk internodes of adult plants]. cDNA was prepared from  
polyA+ mRNA using Superscript Plasmid System Kit  
(Invitrogen). The double-strand cDNAs were fractionated  
in a sepharose CL-2B 40cm-columns and fragments sizing  
between 0.8 and 1.5 Kb were directionally cloned into the  
vector. Details of each source of RNA and library  
construction can be obtained at  
http://sucest.lad.ic.unicamp.br/public"

ORIGIN  
Query Match 38.7%; Score 659.4; DB 6; Length 879;  
Best Local Similarity 91.4%; Pred. No. 9.2e-175;  
Matches 731; Conservative 0; Mismatches 64; Indels 5; Gaps 3;

QY 17 ATCCGAGCCACAGTCTCTCTCGGGCCACCGCGTCCGACCGCGGATGGCAAGACCCC 76  
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DB 27 ATCTGACGACGAGTCTCTACTCGGGCCCGCGCGTCCGCCCGGCGATGGCGAAGCCCC 86  
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QY 77 GTCGTCGCGGTGGCG--GCGGTGCGCGGAGGCGCGGCGCGGCGGTTCAACACCGGACCCA 133  
|||||  
DB 87 GTCGTCGCGGCGGCGGAGCGGTGCGCGGAGGCGCGGCGGCGGTTCAACACCGGACCGG 146  
|||||

QY 134 GTCCT 193  
|||||  
DB 147 GTCCT 206  
|||||

QY 194 CCGCGGTGCGGCGGAGTCCCTCGGGTTTCATGAGTCCAGGTCGAGTCCGCGCCGCGCCCTCAACACCGC 253  
|||||  
DB 207 CCGCGGTGCGGCGGAGTCCCTCGGGTTTCATGAGTCCAGGTCGAGTCCGCGCCGCGCCCTCAACACCGC 266  
|||||

QY 254 CGTCGCGGCGGCGGAGTCCCTCGGGTTTCATGAGTCCAGGTCGAGTCCGCGCCGCGCCCTCAACACCGC 313  
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DB 267 CGTCGCGGCGGCGGAGTCCCTCGGGTTTCATGAGTCCAGGTCGAGTCCGCGCCGCGCCCTCAACACCGC 326  
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QY 314 TGAGCTCTCCCT 373  
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DB 327 CGAGCTCTCCCT 386  
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QY 374 TGTGGCTCGCAAGTGGTGTGGATTAACAAACAGAGATCAACAAGAAACAAATGATGTAC 433  
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Db 387 TGTGGCTCGCAAGTGGTGTGGTAAACAAACAGAGATCAGAAGAAACAAATGATGTAC 446  
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QY 434 ATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTACCAGCTAGAGGACA 493  
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Db 447 ATATAGCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTACCAGTTAGGGGACA 506  
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QY 494 GGAGCGAGTTGATATTGCTCTAAAGAGCTGATCTGGTTATCTTAAACACTGCTGTGCTGG 553  
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Db 507 GGAGCGAGTTGATATTGCTCTGAAGAGCTGATCTGGTTATTNTAAACACTGCTGTGCTGG 566  
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QY 554 CAAGTGGCTTGACCTGTTCTGAAGAGATCATGTTCCCTAAAGTCCTTCCGAAGATTTTGTG 613  
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Db 567 CAAGTGGCTTGATCTGTTCTGAAGAGATCATGTTCCCTAAAGTCCTTNCGAAGATTTTGTG 626  
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QY 614 GTGATCCATGAAATCGTGGCATTTACTTTAAGTTGAATATGTCAAACATCTTCCCTT 673  
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Db 627 GTGATCCATGAAATCGGAGGCGATTTACTTTAAGTTGAATATGTCAAACATCTTCCCTT 686  
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QY 674 TGTGCTGGAGCCATGATTGATTTCTCATACAAC-GGCTGAGTATTGGAATAGCAGGACTA 732  
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Db 687 TGTGCTGGAGCCATGATTGATTTCTTATACACGGGCTTGATATTGGGAGAGCANGACTA 746  
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QY 733 GCGATCGCTGAAATACAGATGCCACAAACTTATGTTGTTACCTGCGGGAATAGTAAAG 792  
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Db 747 GCAACCGGCTTGAAATACAGATGCCACAACTTATTTTGT-ACCTGGGGATATTTTAG 805  
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QY 793 AACTAATGGAAGTTGCTGAA 812  
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Db 806 AACTAATGGAAGTTGCTGAA 825  
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RESULT 11  
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DEFINITION CB661667 831 bp mRNA linear EST 09-APR-2003  
clone OSJNEd04009 5', mRNA sequence.  
ACCESSION CB661667  
VERSION CB661667.1 GI:29665392  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
REFERENCE 1 (bases 1 to 831)  
AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,  
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,  
Soderlund,C. and Wang,G.L.  
TITLE Large-scale identification of expressed sequence tags involved in  
rice and rice blast fungus interaction  
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)  
PUBMED 15888683  
COMMENT Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: gta aac agc tat gac cat g  
BACKWARD: gga aac agc tat gac cat g  
Plate: 04 row: O column: 09  
Seq primer: gta aac cga cgg cca gtg.  
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/dev_stage="3 week"
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/clone_lib="OSJNEB"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match      38.6%; Score 656.8; DB 6; Length 831;
Best Local Similarity 87.0%; Pred. No. 4.9e-174;
Matches 721; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 236 CGCGCCCTCAACACCGCGTCGCCAGCGGAGTCCCTCGGTTTCATGAGGTCCAAGCT 295
Db 3 CGCGACCCCGCACCGCGCGCTCGCAGGGAACCCCTCGAGTTCATGAGGTCCAAGCT 62

QY 296 CGTGCTCTCGTCTCCCATGAGCTCTCCCTCTCTGGTGGTCCACTTTTACTGATGAATT 355
Db 63 CATGCTGCTGCTCTCCACGAGCTCTCCCTCTCCGGGGGACCATGTTACTGATGGAGTT 122

QY 356 AGCATTTCTTCTGAGGCATGTTGGCTCGCAAGTGGTGTGGATAACAAACAGAGATCACA 415
Db 123 GGCATTTCTTCTGCGGCAGGTTGGTTCGCAAGTGGTGTGGATAACAAACAGAGATCGGA 182

QY 416 AGAAACAAATGATGTACATATAGCTTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGT 475
Db 183 AGAAACAAATGATGTTACATATAGCTTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGT 242

QY 476 TTTACCAGCTPAGAGGACAGGAGGAGTTCATATGCTCTAAAAGCTGATCTGGTTATCTT 535
Db 243 ATTACCTGCTAGGGGACATGAGGCGATTGATAGTCCCTAAAGGCTGATCTTGTATCTT 302

QY 536 AAACACTGCTGTGCTGGCAAGTGGCTTGACCCTGTTCTGAAAGATCATGTTCTCTAAAGT 595
Db 303 GAACACTGCTGTGCTGGCAAGTGGCTTGATGCTGTCTCTAAATGACCATGTTCCCAAGT 362

QY 596 CTTTCCGAAGATTTTGTGGTGGATCCATGAAATCGTGGGCATTACTTTAAGTTGAATA 655
Db 363 TCTTCCCAAGATTTTGTGGTGGATCCATGAAATCGGAGGCACTTACTTTAAGCTTGAATA 422

QY 656 TGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGATTTCTCATACAACGGCTGAGTA 715
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QY 716 TTGGAATAGCAGGACTAGCGATCGCTGAAATACAGATGCCACAACTTATGTTGTTCA 775
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Db 603 ACGGAGCATATCCGTGAGTTCCTTGGAGTACGGAGTGAAGATCTTGTGTTTGAATAAT 662

QY 896 AAACAGTGTATCAGGAGAAAGGGACAAGCTTATTTCTTCAAGCATTTTATCAGGCTTT 955
Db 663 AAACAGTGTTCACGTGGAAAGGGCAGGACTTATTTCTTCAAGCGTTTATCAGGCTGT 722

QY 956 GCAGCTCATCCACACGAGAAACTTAAAGTGCTAGATAACATGCTGTAGTTGTGGGAAG 1015
Db 723 CCAGCTCATCGAACAGAAGAAAGTTAAAGTGCCCAATGCATGCTGTAGTTGTGGGAAG 782

QY 1016 TGATGTTAATGCTCAGACCAAATTTGAGACTCAGTTACGTGACTTTGTG 1064
Db 783 TGACATAAATGCTCAGACCNAGTTTGAAGACAAATACGTGATTTTTCG 831
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RESULT 12
CD435900      675 bp      mRNA      linear      EST 03-JUN-2003
LOCUS
DEFINITION   EL01N0367F09.b EndospERM_3 Zea mays cDNA, mRNA sequence.
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ACCESSION      CD435900
VERSION        CD435900.1  GI:31351543
KEYWORDS       EST.
SOURCE         Zea mays
ORGANISM       Zea mays
REFERENCE      1 (bases 1 to 675)
AUTHORS        Lai,J., Dey,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F.,
                Larkins,B., Becraft,P. and Messing,J.
TITLE          Characterization of the maize endosperm transcriptome and its
                comparison to the rice genome
JOURNAL        Genome Res. 14 (10), 1932-1937 (2004)
PUBMED         15466291
COMMENT        Contact: Lai, Jinsheng
                Dr. Joachim Messing's lab
                Waksman Institute, Rutgers University
                190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
                Tel: 732-445-3801
                Fax: 732-445-5735
                Email: jlai@waksman.rutgers.edu
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ORIGIN
Query Match      38.2%; Score 650.2; DB 6; Length 675;
Best Local Similarity 99.4%; Pred. No. 3.4e-172;
Matches 663; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 575 GAAAGATCATGTTCTTAAAGTCTTCCGAAGATTTTGTGGTGGATCCATGAAATCGGTGG 634
Db 9 GATAGATCATGTTCTTAAAGTCTTCCGAAGATTTTGTGGTGGATCCATGAAATCGGTGG 68

QY 635 GCATTACTTTAAGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGA 694
Db 69 GCATTACTTTAAGTTGAATATGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGA 128

QY 695 TTCTCATACAACCGCTGAGTATTGGAATAGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGA 754
Db 129 TTCTCATACAACCGCTGAGTATTGGAATAGTCAAACATCTTCCCTTTGTTGCTGGAGCCATGATTGA 188

QY 755 GCCACAAACTTATGTTGTTTCCCTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGA 814
Db 189 GCCACAAACTTATGTTGTTTCCCTGGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAGA 248

QY 815 CAATGTCGCAAGAGAGTCTCTACGGGAACATATTCGTGAATCCCTTTGGAGTACGGAGTGA 874
Db 249 CAATGTCGCAAGAGAGTCTCTACGGGAACATATTCGTGAATCCCTTTGGAGTACGGAGTGA 308

QY 875 GGATCTCCTGTTTGAATAATAAACAGTGTATCACGAGGAAAGGGACAAGACTTATTTCT 934
Db 309 GGATCTCCTGTTTGAATAATAAACAGTGTATCACGAGGAAAGGGACAAGACTTATTTCT 368

QY 935 TCAAGCATTTTATCAGGCTTTGCAGCTCATCCAAACAGAGAACTTAAAGTGCCTAGAAAT 994
Db 369 TCAAGCATTTTATCAGGCTTTGCAGCTCATCCAAACAGAGAACTTAAAGTGCCTAGAAAT 428

QY 995 ACATGCTGTAGTTGTGGGAAGTGTGATGTTAATGCTCAGACCAAATTTGAGACTCAGTTACG 1054
Db 429 ACATGCTGTAGTTGTGGGAAGTGTGATGTTAATGCTCAGACCAAATTTGAGACTCAGTTACG 488

QY 1055 TGACTTTTGTGTTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAGACATTTGGC 1114
Db 1114 TGACTTTTGTGTTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAGACATTTGGC 1114
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Db 489 TGACTTTTGGTGAAGAACACGATTTCATGACCGTGTCCATTTTGTGAACAAGACATTGGC 548
QY 1115 AGTGGCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAAATTCAGGGCCGTGGAGA 1174
Db 549 AGTGGCCCTTACTTGGCAGCAATTGATGTGCTTGTTCATAATTCAGGGCCGTGGAGA 608
QY 1175 ATGCTTTGGAAGGATAACAATTGAAGCAA-TGGCATTCAAGTTGCCAGTATTGGGCACGG 1233
Db 609 ATGCTTTGGAAGGATAACAATTGAAGCAAATGGCAATGGCAATTCAGTTGCCAGTATTGGGCACGG 668
QY 1234 CTGCTGG 1240
Db 669 CTGCTGG 675

RESULT 13
CB660163
LOCUS
DEFINITION
OSJNEd01K22.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEd01K22 5', mRNA sequence.
ACCESSION
CB660163
VERSION
CB660163.1 GI:29663888
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 813)
Jantassuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 01 row: K column: 22
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1. .813
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEd01K22"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEd"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match 37.9%; Score 645.8; DB 6; Length 813;
Best Local Similarity 87.9%; Pred. No. 6.4e-171;
Matches 715; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 419 AACAAATGATGTCACATATA-GCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGTTT 477
Db 1 AACAAATGATGTTACATCTATTCTTGGAGCATAGATGTTGAGCCATGGAGTGCAGGTAT 60
QY 478 TACCAGCTAGAGGACAGGAGGCAGTTGATATTGCTCTAAAGCTGATCTGTTATCTTAA 537
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Db 61 TACCTGTAGGGGACATGAGGCGATTGATCTGCCCTAAAGGCTGATCTTGTATCTTGA 120
QY 538 ACACCTGCTGTGCTGGCAAGTGGCTTGGACCCCTGTTCTGAAAGATCATGTTCTCTAAAGTCC 597
Db 121 ACACCTGCTGTGCTGGCAAGTGGCTTGGATGCTGTCTCTAAATGACCATGTTCTCCCAAGTTC 180
QY 598 TTCCGAAGATTTTGTGGTGGATCCATGAAATGCGTGGGCATTACTTTAAAGTTGAATATG 657
Db 181 TTCCCAAGATTTTGTGGTGGATCCATGAAATGCGAGGGCATTACTTTAAGCTTGAATATG 240
QY 658 TCAACATCTTCCCTTTGTTGCTGGAGCCCATGATTGATCTCTATACAACGGCTGAGTATT 717
Db 241 TCAACATCTTCCCTCTGTTGCTGGAGCCCATGATTGATCTCTATACAACGGCTGAGTATT 300
QY 718 GGAATAGCAGGACTAGCGATCGCTGAAATAACAGATGCCACAACCTTATGTTGTTCAAC 777
Db 301 GGAAGACCAGGACTCATGACCGTTTGAATAATACAGATGCCACAACCTTATGTTGTTCAAC 360
QY 778 TGGGAATAGTAAAGAACTAATGGAAGTTGCTGAAAGACAATGTCGCAAGAGAGTCTCTAC 837
Db 361 TCGGGAATAGTAAGGAGTTAATGGAAGTTGCTGAAGATAATGTTGCAAGAAGAGTCTCTAC 420
QY 838 GGAACATATTTCGTGAATCCCTTGGAGTACGGAGTACGAGTCTCTGTTTGCATAATAA 897
Db 421 GGGAGCATATCCGTGAGTTCTTGGAGTACGGAGTACGAGTCTTGTGTTTGCATAATAA 480
QY 898 ACAGTGTATCACGAGGAAAGGACAAGACTTATTTCTTCAAGCATTTTATCAGGCTTTGC 957
Db 481 ACAGTGTTCACGTGGAAAGGCGAGGACTTATTTCTTCAAGCGTTTATCAGGCTGTC 540
QY 958 AGCTCATCCAACACGAGAAACTTAAAGTCCCTAGATACATGCTGTAGTTGTGGGAAGTG 1017
Db 541 AGCTCATCGAACAGAAAGTTAAAGTGCCCAACAATGCAATGCTGTAGTTGTGGGAAGTG 600
QY 1018 ATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGCTTGTGGTGAAGAACACGA 1077
Db 601 ACATAAATGCTCAGACCAAGTTTGAGACACAATTACGTGATTTGCGGTGAAGAATGGGA 660
QY 1078 TTCATGACCGTGTCCATTTTGTGAACAAGACATTTGGCAGTGGCCCTTACTTTGGCAGCAA 1137
Db 661 TTCAGGACCGGTTTCACITTTGTAAACAAGACATTAGCAGTGGCTCTTATTTGGCTGCAA 720
QY 1138 TTGATGTGCTTGTTCAGAAATTTCTCAGGGCCGCTGGAGAATGCTTTTGAAGGATAACAATTG 1197
Db 721 CTGATGTGCTTGTTCAGAACTCTCAGCCCGCTGGAGAATGCTTTTGAAGGATAACAATTG 780
QY 1198 AAGCAATGGCATTCAAGTTGCCAGTATTGGGCA 1230
Db 781 AAGCAATGGCATTCAAGTTGCCAGTATTGGGCA 813

RESULT 14
CO448834
LOCUS
DEFINITION
MZCCL10129H06.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA
sequence.
ACCESSION
CO448834
VERSION
CO448834.1 GI:67020085
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 753)
REFERENCE
Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and
Arruda,P.
Endosperm-preferred expression of maize genes as revealed by
transcriptome-wide analysis of expressed sequence tags
Plant Mol. Biol. (2005) In press
Contact: Arruda P
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each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match		36.5%	Score 621;	DB 8;	Length 629;
Best Local Similarity		99.2%	Pred. No. 6.2e-164;		
Matches	624;	Conservative	0;	Mismatches	5;
				Indels	0;
				Gaps	0;
QY	998	TGCTGTAGTTCTGGGAAGTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGA	1057		
Db	629	TGCTGTAGTTCTGGGAAGTGATGTTAATGCTCAGACCAAAATTTGAGACTCAGTTACGTGA	570		
QY	1058	CTTTGTGGTGAAGAACACGATTTCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGT	1117		
Db	569	CTTTGTGGTGAAGAACACGATTTCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGT	510		
QY	1118	GGCCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAATTCTCAGGGCCCGTGGAGAATG	1177		
Db	509	GGCCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAATTCTCAGGGCCCGGGAATG	450		
QY	1178	CTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTTGGCACGGCTGC	1237		
Db	449	CTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTTGGCACGGCTGC	390		
QY	1238	TGGAGGGACACGAGATCGTCTGGACGGCTCGACTGGCCTTCTGCATCCTGCTGGAA	1297		
Db	389	TGGAGGGACACGAGATCGTCTGGACGGCTCGACTGGCCTTCTGCATCCTGCTGGAA	330		
QY	1298	GGAGGGCGTGGCGCCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAG	1357		
Db	329	GGAGGGCGGGCGCCTCTTGCAAAGAACATCGTCAGACTCCCAAGCCACGCCGAGCAGAG	270		
QY	1358	GGTCTCCATGGGGGAAAGGGCTATGGCAGGGTGAAGGAATGTTTCATGGAGCACCACAT	1417		
Db	269	GGTCTCCATGGGGGAAAGGGTTATGGCAGGGTGAAGGAATGTTTCATGGAGCCCCACAT	210		
QY	1418	GGCTGAGAGGATCGCGCGGTGTTGAAGGATGCTCTGAGGAAATCACAGGAGCAGTCCAG	1477		
Db	209	GGCTGAGAGGATCGCGCGGTGTTGAAGGATGCTCTGAGGAAATCACAGGAGCAGTCCAG	150		
QY	1478	GTCTTGAGCTTTGCCGTGCCCATCAGCTTGGCTAACATGTTGAAGTATGTTTACGGGC	1537		
Db	149	GTCTTGAGCTTTGCCGTGCCCATCAGCTTGGCTAACATGTTGAAGTATGTTTACGGGC	90		
QY	1538	TACGCCTACGTGGTTCAGGCTGTAACTGTAGATTGCACCTCTGTGGTCTACTTTTTCAC	1597		
Db	89	TACGCCTACGTGGTTCAGGCTGTAACTGTAGATTGCACCTCTGTGGTCTACTTTTTCAC	30		
QY	1598	ATTCATGTTTTTACCTATTAGGCCATGTCC	1626		
Db	29	ATTCATGTTTTTACCTATTAGGCCATGTCC	1		

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